

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 8, 2002, 11:46:20 ; Search time 10.16 Seconds
(without alignments)
57.740 Million cell updates/sec

Title: US-09-647-457-2

Perfect score: 16

Sequence: 1 LVYGLCTCQIKTGPAC 16

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 100059 seqs, 36664827 residues

Word size: 0

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SWISSProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	43.8	335	1 MPBL_HUMAN	P22712 homo sapien
2	7	43.8	395	1 ENO_ALMT	P42897 alligator m
3	7	43.8	433	1 ENOA_ANAPL	P19140 anas platyr
4	7	43.8	433	1 ENOA_BOVIN	O9X514 bos taurus
5	7	43.8	433	1 ENOA_CHICK	P51913 gallus gall
6	7	43.8	433	1 ENOA_HUMAN	P06733 homo sapien
7	7	43.8	433	1 ENOA_MOUSE	P17182 mus musculu
8	7	43.8	433	1 ENOA_RAT	P04764 rattus norv
9	7	43.8	433	1 ENOA_CHICK	P13929 homo sapien
10	7	43.8	433	1 ENOA_HUMAN	P21550 mus musculu
11	7	43.8	433	1 ENOA_MOUSE	P25704 onychotagus
12	7	43.8	433	1 ENOA_RABIT	P15429 rattus norv
13	7	43.8	433	1 ENOA_HUMAN	P09104 homo sapien
14	7	43.8	433	1 ENOA_MOUSE	P17183 mus musculu
15	7	43.8	433	1 ENOG_MOUSE	P07323 rattus norv
16	7	43.8	433	1 ENOG_RAT	P56252 homarus gam
17	7	43.8	433	1 ENO_HONGA	P08734 xenopus lae
18	7	43.8	433	1 ENO_XENLA	O02654 loligo peal
19	7	43.8	434	1 ENO_SCHUA	P33676 schistosoma
20	7	43.8	434	1 ENO_SCHUA	O21871 schistosoma
21	7	43.8	434	1 ENO_SCHUA	O05524 homo sapien
22	7	43.8	434	1 ENO_SCHUA	P11896 pleurodeles
23	7	43.8	434	1 ENO_SCHUA	O58888 methanococ
24	7	43.8	434	1 ENO_SCHUA	O15746 dictyostell
25	7	43.8	434	1 ENO_SCHUA	O25964 helicobact
26	7	43.8	434	1 ENO_SCHUA	P74931 treponema p
27	7	43.8	434	1 ENO_SCHUA	O92365 schistosacch
28	7	43.8	434	1 ENO_SCHUA	O94658 schistosacch
29	7	43.8	434	1 ENO_SCHUA	O95252 sus scrofa
30	7	43.8	434	1 ENO_SCHUA	P80306 rhododactyl
31	7	43.8	434	1 ENO_SCHUA	P19044 zea mays (m
32	7	43.8	434	1 ENO_SCHUA	
33	7	43.8	434	1 ENO_SCHUA	

34	5	31.2	120	1 NU3C_ORYSA	P12126 oryza sativ
35	5	31.2	120	1 NU3C_WHEAT	P26303 triticum ae
36	5	31.2	134	1 RL27_PVRST	O02984 pyrobolrys
37	5	31.2	152	1 YF47_STMY3	P74662 synecocyst
38	5	31.2	157	1 YSA4_ECOLI	P56256 escherichia
39	5	31.2	169	1 LSHB_HORSE	P08751 equus cabal
40	5	31.2	172	1 NU6M_CYPCA	P24982 cyprius ca
41	5	31.2	173	1 NU6M_AETPY	P43191 aethia pygm
42	5	31.2	173	1 NU6M_CARAU	O78689 carassius a
43	5	31.2	173	1 NU6M_FRACR	P43201 fratercula
44	5	31.2	173	1 NU6M_LATICH	O03175 latimeria c
45	5	31.2	173	1 NU6M_PTYAL	P43203 ptychoramph

ALIGNMENTS

RESULT 1	MPBL_HUMAN	STANDARD;	PRT;	335 AA.
AC	P22712:			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	C-MYC PROMOTER-BINDING PROTEIN (MPB-1) (MBP-1).			
GN	MPB1 OR MBP1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91172204; PubMed=2005901;			
RA	Ray R., Miller D.M.;			
RT	Cloning and characterization of a human c-myc promoter-binding			
RT	protein.			
RL	Mol. Cell. Biol. 11:2154-2161(1991).			
CC	FUNCTION: BINDS TO THE C-MYC PROMOTER REGION OF THE C-MYC GENE			
CC	AND IS THOUGHT TO REPRESS TRANSCRIPTION.			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).			
CC	-1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
DR	EMBL: M55914; AAA35698.1; -			
DR	PIR: A39579; A39579.			
DR	HSSP: P56252; IPDY.			
DR	TRANSFAC: T00498; -			
DR	MTM: 602456; -			
DR	InterPro: IPR000941; Enolase.			
DR	Pfam: PF00113; enolase; 2.			
DR	Prodom: PD000902; Enolase; 1.			
DR	PROSITE: PS00164; ENOLASE; FALSE_NEG.			
KW	DNA-binding; Transcription regulation; Repressor; Nuclear protein.			
SQ	SEQUENCE 335 AA; 37087 MW; B63ADD7A67AE0A CRC64;			

Query Match 43.8%; Score 7; DB 1; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVYGLCT 7
Db 285 LVYGLCT 291

RESULT 2

ENCL1MT
ID ENCL1MT STANDARD: PRT: 395 AA.
AC P42897;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ENCL1MT (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Crocodylia; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94195794; PubMed=8146164;
RA "Molecular evidence for the origin of birds."
RT Proc. Natl. Acad. Sci. U.S.A. 91:2621-2624(1994).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H₂O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
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CC -----
DR EMBL: L28078; AAAS3671.1; -.
DR HSSP: P56252; LPDY.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR ProDom: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW Lyase; Glycolysis; Magnesium.
FT METAL 1 136 136 BY SIMILARITY.
FT METAL 223 223 MAGNESIUM (BY SIMILARITY).
FT METAL 271 271 MAGNESIUM (BY SIMILARITY).
FT METAL 296 296 MAGNESIUM (BY SIMILARITY).
FT NON_TER 395 395
SQ SEQUENCE 395 AA; 42884 MW; BA3E91228E9110B5 CRC64;
Query Match 43.8%; Score 7; DB 1; Length 395;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVVGICT 7
Db 362 LVVGICT 368
RESULT 3
ENCL1MT ANAPL STANDARD: PRT: 433 AA.
AC P19140;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (TAU-CRYSTALLIN).
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89079778; PubMed=2462567;
RA Wislow G.J., Liehman T., Williams L.A., Stapel S.O., de Jong W.W., Horwitz J., Platigorsky J.;
RT "Tau-crystallin/alpha-enolase-one gene encodes both an enzyme and a lens structural protein."
RT J. Cell Biol. 107:2729-2736(1988).
CC -1- FUNCTION: BOTH AN ENZYME AND A LENS STRUCTURAL PROTEIN.
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H₂O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
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CC -----
DR EMBL: M20749; AAA49218.1; -.
DR EMBL: X14195; CAA32409.1; -.
DR PIR: A32132; A32132.
DR HSSP: P56252; LPDY.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR PRINTS: PR00148; ENOLASE.
DR ProDom: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW Lyase; Glycolysis; Magnesium; Eye lens protein.
FT INIT_MET 0 0
FT ACT_SITE 157 157
FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 433 AA; 47108 MW; 1AED78B08A6E8AD CRC64;
Query Match 43.8%; Score 7; DB 1; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVVGICT 7
Db 383 LVVGICT 389
RESULT 4
ENCL1MT BOVIN STANDARD: PRT: 433 AA.
AC O9X574;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-NEURAL ENOLASE) (NNE) (PHOSPHOENOLPYRUVATE DEHYDRATASE).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovidae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Chapman K.L., Newman B., Hillaby M.C., Freemont A.J., Grant M.E., Boot-Handford R., Wallis G.A.;

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RT "Alpha enolase is upregulated in proliferative chondrocytes in the
RT epiphyseal growth plate and in human osteoarthritic tissue.";
RT Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
CC + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
CC IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
CC MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
CC FOUND ONLY IN NERVOUS TISSUE.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
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CC or send an email to license@isb-sib.ch).
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CC EMBL: AF149256; AAD33073.1; -.
CC HSSP: P56252; 1PDZ.
CC InterPro: IPR000941; Enolase.
CC Pfam: PF00113; enolase.1.
CC PRINTS: PR00148; ENOLASE.
CC Kyr: Glycolysis; Magnesium; Multigene family.
CC Lys: Glycolysis; Magnesium; Multigene family.
CC ACT_SITE 157 157 0 BY SIMILARITY.
CC METAL 244 244 MAGNESIUM (BY SIMILARITY).
CC METAL 292 292 MAGNESIUM (BY SIMILARITY).
CC METAL 317 317 MAGNESIUM (BY SIMILARITY).
CC METAL 317 317 MAGNESIUM (BY SIMILARITY).
CC SEQUENCE 433 AA; 47145 MW; B004E965C46F2E0C CRC64;

Query Match 43.8%; Score 7; DB 1; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVGLICT 7
DB 383 LVGLICT 389

RESULT 5
ENOA_CHICK STANDARD; PRT; 433 AA.
ID ENOA_CHICK
AC P51913;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
DE (PHOSPHOPYRUVATE HYDRATASE).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CC NCBI_TaxID=9031;
CC
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=WHITE LEGHORN; TISSUE=Kidney;
CC MEDLINE=95355305; PubMed=7629021;
CC Tanaka M., Maeda K., Nakashima K.;
CC "Chicken alpha-enolase but not beta-enolase has a Src-dependent
CC tyrosine-phosphorylation site: cDNA cloning and nucleotide sequence
CC analysis.";
CC J. Biochem. 117:554-559(1995).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
CC + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING

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CC THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
-----
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-----
CC EMBL: D37900; BAA07132.1; -.
CC HSSP: P56252; 1PDZ.
CC InterPro: IPR000941; Enolase.
CC Pfam: PF00113; enolase.1.
CC PRINTS: PR00148; ENOLASE.
CC ProDom: PD000902; ENOLASE.
CC PROSITE: PS00164; ENOLASE.1.
CC Kyr: Glycolysis; Magnesium; Multigene family.
CC Lys: Glycolysis; Magnesium; Multigene family.
CC ACT_SITE 157 157 0 BY SIMILARITY.
CC METAL 244 244 MAGNESIUM (BY SIMILARITY).
CC METAL 292 292 MAGNESIUM (BY SIMILARITY).
CC METAL 317 317 MAGNESIUM (BY SIMILARITY).
CC SEQUENCE 433 AA; 47173 MW; 93AD6B0A7AD99910 CRC64;

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Query Match 43.8%; Score 7; DB 1; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LVGLICT 7
DB 383 LVGLICT 389

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RESULT 6
ENOA_HUMAN STANDARD; PRT; 433 AA.
ID ENOA_HUMAN
AC P06733; Q16704; Q9UM55;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-
DE NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CC NCBI_TaxID=9606;
CC
CC [1]
CC SEQUENCE FROM N.A.
CC MEDLINE=86313654; PubMed=3529090;
CC Gallongo A., Feo S., Moore R., Croce C.M., Shove L.C.;
CC "Molecular cloning and nucleotide sequence of a full-length cDNA for
CC human alpha enolase.";
CC Proc. Natl. Acad. Sci. U.S.A. 83:6741-6745(1986).
CC [2]
CC SEQUENCE FROM N.A.
CC MEDLINE=90323004; PubMed=2373081;
CC Gallongo A., Oliva D., Cali L., Barba G., Barbieri G., Feo S.;
CC "Structure of the human gene for alpha-enolase.";
CC Eur. J. Biochem. 190:567-573(1990).
CC [3]
CC SEQUENCE FROM N.A.
CC TISSUE=Endometrium;
CC MEDLINE=96422099; PubMed=8824716;
CC Walter M., Leidenberger F.A., Scheppe K.W., Berg H., Northmann W.;
CC "Antireactive epitopes within the human alpha-enolase and their
CC recognition by sera from patients with endometriosis.";

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RL J. Autoimmun. 8:937-945(1995).
 RN [4]
 RP SEQUENCE OF 165-433 FROM N.A.
 RX MEDLINE=98317532; PubMed=9653645;
 RA Onyango P., Lubkova B., Gardellin P., Kurzbauer R., Weith A.;
 RT "Molecular cloning and expression analysis of five novel genes in
 RL chromosome 1p36.";
 RN Genomics 50:187-198(1998).
 RN [5]
 RP SEQUENCE OF 269-280 AND 306-320.
 RX MEDLINE=95307697; PubMed=7787969;
 RA Mohamed R.M., Hamdan M.Y., Maki A., Al-Katib A.;
 RT "Induced expression of alpha-enolase in differentiated diffuse large
 RL cell lymphoma.";
 RN Enzyme Protein 48:37-44(1995).
 RN [6]
 RP SEQUENCE OF 1-8.
 RC TISSUE-Colon carcinoma;
 RX MEDLINE=97295306; PubMed=9150948;
 RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
 RT "A two-dimensional gel database of human colon carcinoma proteins.";
 RL Electrophoresis 18:605-613(1997).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
 CC + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
 CC THE DIMER.
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
 CC IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
 CC MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
 CC FOUND ONLY IN NERVOUS TISSUE.
 CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: M14328; AAA52387.1; -
 DR EMBL: M14388; CAA34360.1; -
 DR EMBL: X16289; CAA34360.1; JOINED.
 DR EMBL: X16290; CAA34360.1; JOINED.
 DR EMBL: X84907; CAA59331.1; -
 DR EMBL: U88968; AAC39935.1; -
 DR PIR: A29170; A29170.
 DR PIR: S11696; S11696.
 DR HSP: P56252; 1PDY.
 DR Aarhus/Ghent-2DPAGE; 1325; IEF.
 DR Aarhus/Ghent-2DPAGE; 5406; NEPHGE.
 DR MIM: 172430; -
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; Enolase.1.
 DR PRINTS: PR00148; ENOLASE.1.
 DR PRODOM: PD000902; Enolase.1.
 DR PROSITE: PS00164; ENOLASE.1.
 KW Lyase; Glycolysis; Magnesium; Multigene family.
 FT INT MET 0
 FT ACT_SITE 157
 FT METAL 244
 FT METAL 292
 FT METAL 317
 FT CONFLICT 251
 FT SEQUENCE 433 AA; 47037 MW; B2028684C33140B5 CRC64;
 Query Match 43.8%; Score 7; DB 1; Length 433;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVGLCT 7
 ID 111111
 Db 383 LVGLCT 389
 RESULT 7
 ENOA_MOUSE STANDARD; PRT; 433 AA.
 AC P17182; O9DCY7;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-
 DE NEURAL ENOLASE) (NNE).
 GN ENO1 OR ENO-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=90301487; PubMed=2362815;
 RA Kaghad M., Dumont X., Chalon P., Lelias J.M., Lamande N., Lucas M.,
 RA Lazar M., Caput D.;
 RT "Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from
 RL mouse brain.";
 RN Nucleic Acids Res. 18:3638-3638(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aekawa T., Hara A., Fukunishi Y., Konno H., Aachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
 RA Kiehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Orido T., Futuno M., Aono H., Baldarelli R., Barish G.,
 RA Blake J., Borrelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombere P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata T., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001)
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
 CC + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
 CC THE DIMER.
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
 CC IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
 CC MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
 CC FOUND ONLY IN NERVOUS TISSUE.
 CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----

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CC -----
CC EMBL: X52379; CAA36605.1; -
CC EMBL: AK002336; BAB22021.1; -
CC PIR: S10246; S10246.
CC HSSP: P56252; LPDY.
CC SWISS-2DPAGE: P17187; MOUSE.
CC MGI: 95393; ENOL.
CC InterPro: IPR000941; Enolase.
CC Pfam: PF00113; enolase; 1.
CC PRINTS: PR00148; ENOLASE.
CC ProDom: PD000902; ENOLASE; 1.
CC PROSITE: PS00164; ENOLASE; 1.
CC KEGG: Glycolysis; Magnesium; Multigene family.
CC INT_MET 0
CC ACT_SITE 157 157 BY SIMILARITY.
CC METAL 244 244 MAGNESIUM (BY SIMILARITY).
CC METAL 292 292 MAGNESIUM (BY SIMILARITY).
CC METAL 317 317 MAGNESIUM (BY SIMILARITY).
CC CONFLICT 358 358 L -> P (IN REF. 1).
CC SEQUENCE 433 AA; 47009 MW; C90082CBA8290EB6 CRC64;

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Query Match 43.8%; Score 7; DB 1; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVVGLCT 7
Db 383 LVVGLCT 389

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RESULT 8
ENOA_RAT STANDARD; PRT; 433 AA.
ID ENOA_RAT
AC P04764;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-NEUTRAL ENOLASE) (NNE).
GN ENO1 OR ENO-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85242108; PubMed=2989793; Sakimura K., Kushiya E., Ohinata M., Takahashi Y.; "Molecular cloning and the nucleotide sequence of cDNA to mRNA for non-neutonal enolase (alpha alpha enolase) of rat brain and liver.", Nucleic Acids Res. 13:4365-4378(1985).
RT [2]
RL SEQUENCE FROM N.A.
RN Takahashi Y.;
RA Submitted (JAN-1986) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS FOUND ONLY IN NERVOUS TISSUE.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC or send an email to license@sb-sib.ch).
CC -----
CC EMBL: X02610; CAA26456.1; -
CC PIR: A23126; A23126.
CC HSSP: P56252; LPDY.
CC InterPro: IPR000941; Enolase.
CC Pfam: PF00113; enolase; 1.
CC PRINTS: PR00148; ENOLASE.
CC ProDom: PD000902; ENOLASE; 1.
CC PROSITE: PS00164; ENOLASE; 1.
CC KEGG: Glycolysis; Magnesium; Multigene family.
CC INT_MET 0
CC ACT_SITE 157 157 BY SIMILARITY.
CC METAL 244 244 MAGNESIUM (BY SIMILARITY).
CC METAL 292 292 MAGNESIUM (BY SIMILARITY).
CC METAL 317 317 MAGNESIUM (BY SIMILARITY).
CC SEQUENCE 433 AA; 46984 MW; F1A25F010C276ETC CRC64;

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Query Match 43.8%; Score 7; DB 1; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVVGLCT 7
Db 383 LVVGLCT 389

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RESULT 9
ENOB_CHICK STANDARD; PRT; 433 AA.
ID ENOB_CHICK
AC P07322;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (PHOSPHOPYRUVATE HYDRATASE).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae.
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN; TISSUE=Muscle;
RX MEDLINE=9535305; PubMed=7629021; Tanaka M., Maeda K., Nakashima K.; "Chicken alpha-enolase but not beta-enolase has a Src-dependent tyrosine-phosphorylation site: cDNA cloning and nucleotide sequence analysis.", J. Biochem. 117:554-559(1995).
RT [2]
RL J. Biochem. 117:554-559(1995).
RN SEQUENCE.
RX MEDLINE=87075592; PubMed=3539098; Russell G.A., Dunbar B., Fothergill-Gilmore L.A.; "The complete amino acid sequence of chicken skeletal-muscle enolase.", Biochem. J. 236:115-126(1986).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC -----

DR EMBL: D37901; BAA07133.1; -

DR PIR: A23850; A23850.

DR HSSP; P56252; 1PDY.

DR InterPro: IPR000941; Enolase.

DR Pfam: PF00113; enolase; 1.

DR PRINTS; PR00148; ENOLASE.

DR ProDom: PD000902; ENOLASE; 1.

DR PROSITE; PS00164; ENOLASE; 1.

KW Lyase; Glycolysis; Magnesium; Multigene family; Acetylation.

FT INIT_MET 0

FT MOD_RES 0

FT ACT_SITE 157 157

FT METAL 244 244

FT METAL 292 292

FT METAL 317 317

FT CONFLICT 16 16

FT CONFLICT 48 48

FT CONFLICT 93 93

FT CONFLICT 118 119

FT CONFLICT 208 208

FT CONFLICT 257 257

FT CONFLICT 265 266

FT CONFLICT 269 269

FT CONFLICT 308 308

FT CONFLICT 322 322

FT CONFLICT 330 330

FT CONFLICT 342 342

FT CONFLICT 393 394

SO SEQUENCE 433 AA; 47065 MW; 9BC2B5FB910C254 CRC64;

Query Match

Best Local Similarity 100.0%; Score 7; DB 1; Length 433;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7

Db 383 LVVGLCT 389

RESULT 10

ENOB HUMAN STANDARD; PRT; 433 AA.

AC P13929; 01-JAN-1990 (Rel. 13, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE BETA ENOLASE (EC 4.2.1.11) (2-PHOSHO-D-GLYCERATE HYDRO-LYASE)

DE (SKELETAL MUSCLE ENOLASE) (MSE).

GN ENO3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_Taxid=9606; [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90067857; PubMed=2567223;

RA Peshavaria M., Hinks L.J., Day I.N.M.;

RT "Structure of human muscle (beta) enolase mRNA and protein deduced from a genomic clone."

RL Nucleic Acids Res. 17:8862-8862(1989).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=91222137; PubMed=1840492;

RA Peshavaria M., Day I.N.M.;

RT "Molecular structure of the human muscle-specific enolase gene (ENO3)."

RL Biochem. J. 275:427-433(1991).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=90245587; PubMed=2336366;

RA Call L., Feo S., Oliva D., Giallongo A.;

RT "Nucleotide sequence of a cDNA encoding the human muscle-specific enolase (MSE)."

RL Nucleic Acids Res. 18:1893-1893(1990).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=93292497; PubMed=8513787;

RA Giallongo A., Venturilla S., Oliva D., Barbieri G., Rubino P., Feo S.;

RT "Structural features of the human gene for muscle-specific enolase. Differential splicing in the 5'-untranslated sequence generates two forms of mRNA."

RL Eur. J. Biochem. 214:367-374(1993).

CC -1- CATALYTIC ACTIVITY: 2-PHOSHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.

CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER.

CC -1- PATHWAY: GLYCOLYSIS.

CC -1- SUBUNIT: HOMODIMER.

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.

CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS FOUND ONLY IN NERVOUS TISSUE.

CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.

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CC -----

DR EMBL: X16504; CAA34513.1; -

DR EMBL: X51957; CAA36216.1; -

DR EMBL: X55976; CAA39446.1; -

DR EMBL: X56832; CAA40163.1; -

DR PIR: S15933; S15933.

DR PIR: S06756; S06756.

DR PIR: S14759; S14759.

DR PIR: S31650; S31650.

DR PIR: S33330; S33330.

DR HSSP; P56252; 1PDY.

DR MIM; 131370; -

DR InterPro: IPR000941; Enolase.

DR Pfam; PF00113; enolase; 1.

DR PRINTS; PR00148; ENOLASE.

DR ProDom; PD000902; ENOLASE; 1.

DR PROSITE; PS00164; ENOLASE; 1.

KW Lyase; Glycolysis; Magnesium; Multigene family.

FT INIT_MET 0

FT ACT_SITE 157 157

FT METAL 244 244

FT METAL 292 292

FT METAL 317 317

FT CONFLICT 84 84

FT CONFLICT 161 161

SO SEQUENCE 433 AA; 46855 MW; 5F726D743DEB82F CRC64;

Query Match

Best Local Similarity 100.0%; Score 7; DB 1; Length 433;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7

Db 383 LVVGLCT 389

RESULT 11

ENOB_MOUSE
ID ENOB_MOUSE STANDARD: PRT: 433 AA.
AC P2150;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
DE (SKELETAL MUSCLE ENOLASE).
ENOB OR ENO-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=Liver;
RA Lamande N., Brosset S., Keller A., Lucas M., Lazar M.;
RL Submitted (SEP-1991) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H;
RX MEDLINE=92290133; PubMed=1339335;
RA Peterson C.A., Cho M., Rastinejad F., Blau H.M.;
RT "Beta-enolase is a marker of human myoblast heterogeneity prior to
differentiation";
RL Dev. Biol. 151:626-629(1992).
RN [3]
RP SEQUENCE OF 58-433 FROM N.A.
RX MEDLINE=89282789; PubMed=2734297;
RA Lamande N., Mazo A.M., Lucas M., Montarras D., Pliset C., Gros F.,
RA Legault-Demare L., Lazar M.;
RT "Murine muscle-specific enolase: cDNA cloning, sequence, and
developmental expression";
RL Proc. Natl. Acad. Sci. U.S.A. 86:4445-4449(1989).
CC --1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
+ H(2O).
CC --1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
THE DIMER.
CC --1- PATHWAY: GLYCOLYSIS.
CC --1- SUBUNIT: HOMODIMER.
CC --1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC --1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
FOUND ONLY IN NERVOUS TISSUE.
CC --1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X61600; CAA43797.1; -
CC EMBL: X62667; AAA44540.1; -
CC EMBL: M20745; AAA37554.1; -
CC EMBL: X57747; CAA40913.1; -
CC PIR: S17109; NQMSB.
CC PIR: A33921; A33921.
CC PIR: S29675; S29675.
CC HSSP: P56252; 1PDY.
CC SWISS-2DPAGE: P21550; MOUSE.
CC MGD: MGI:95395; Eno3.
CC InterPro: IPR000941; Enolase.
CC Pfam: PF00113; enolase.1.
CC PRINTS: PR00148; ENOLASE.
CC PRODOM: PD000902; Enolase; 1.
CC PROSITE: PS00164; ENOLASE; 1.
CC Lysase; Glycolysis; Magnesium; Multigene family.
FT INIT MET 0
FT ACT_SITE 157 157 BY SIMILARITY.

FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
FT CONFLICT 233 234 AG -> NA (IN REF. 3).
SQ SEQUENCE 433 AA; 46893 MW; B31B576382D3FA8 CMC64;
Query Match 43.8%; Score 7; DB 1; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LVVGLCT 7
DB 383 LVVGLCT 389
RESULT 12
ENOB_RABBIT STANDARD: PRT: 433 AA.
AC P25704; O9N0N6;
DT 01-MAY-1992 (Rel. 22, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
DE (SKELETAL MUSCLE ENOLASE).
ENOB.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=9113295; PubMed=2275753;
RA Chin C.C.O.;
RT "The primary structure of rabbit muscle enolase";
RL J. Protein Chem. 9:427-432(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Zheng S.-X.;
RT "The cDNA cloning of rabbit muscle-specific enolase gene, site
directed mutagenesis (R417L) of the gene, expression of the wild-type
and mutant genes in Escherichia coli";
RL Thesis (1995), Concordia University, Montreal / Quebec, Canada.
CC --1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
+ H(2O).
CC --1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
THE DIMER.
CC --1- PATHWAY: GLYCOLYSIS.
CC --1- SUBUNIT: HOMODIMER.
CC --1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC --1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
FOUND ONLY IN NERVOUS TISSUE.
CC --1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF260259; AAF71925.1; -
CC PIR: A37210; A37210.
CC HSSP: P56252; 1PDY.
CC InterPro: IPR000941; Enolase.
CC Pfam: PF00113; enolase.1.
CC PRINTS: PR00148; ENOLASE.
CC PRODOM: PD000902; Enolase; 1.
CC PROSITE: PS00164; ENOLASE; 1.

Lyase; Glycolysis; Magnesium; Multigene family.
 KW INIT_MET 0
 FT ACT_SITE 157 157 BY SIMILARITY.
 FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
 FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
 FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
 FT CONFLICT 253 253 N -> D (IN REF. 1).
 FT CONFLICT 296 296 N -> D (IN REF. 1).
 SQ SEQUENCE 433 AA; 46859 MW; 063A4005443C0403 CRC64;

Query Match 43.8%; Score 7; DB 1; Length 433;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVGIGCT 7
 Db 383 LVGIGCT 389

RESULT 13
 ENOB_RAT
 ID ENOB_RAT STANDARD; PRT; 433 AA.
 AC P15429;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
 DE (SKELETAL MUSCLE ENOLASE).
 GN ENO3 OR ENO-3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar;
 RX MEDLINE=8912113; PubMed=2914621;
 RA Oshima Y., Mitsui H., Takayama Y., Kushiya E., Sakimura K.,
 RA Takahashi Y.;
 RT "CDNA cloning and nucleotide sequence of rat muscle-specific enolase
 (beta beta enolase).";
 RL FEBS Lett. 242:425-430(1989).
 RN [2]
 RP SEQUENCE OF 1-27 FROM N.A.
 RX MEDLINE=91099531; PubMed=2269373;
 RA Sakimura K., Kushiya E., Onshima-Ichimura Y., Mitsui H.,
 RA Takahashi Y.;
 RT "Structure and expression of rat muscle-specific enolase gene";
 RL FEBS Lett. 277:78-82(1990).
 RT -1 CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
 + H(2)O.
 CC -1 COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
 THE DIMER.
 CC -1 PATHWAY: GLYCOLYSIS.
 CC -1 SUBUNIT: HOMODIMER.
 CC -1 SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1 TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
 IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
 MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
 FOUND ONLY IN NERVOUS TISSUE.
 CC -1 SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 DR EMBL; Y00979; CA68788.1; -
 DR EMBL; X57774; CAA40920.1; -;

DR PIR: S02072; S02072.
 DR HSSP; P56252; IPDY.
 DR InterPro; IPR000941; Enolase.
 DR Pfam; PF00113; enolase; 1.
 DR PRINTS; PR00148; ENOLASE.
 DR ProDom; PD000902; Enolase; 1.
 DR PROSITE; PS00164; ENOLASE; 1.
 KW Lyase; Glycolysis; Magnesium; Multigene family.
 FT INIT_MET 0
 FT ACT_SITE 157 157 BY SIMILARITY.
 FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
 FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
 FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 433 AA; 46829 MW; 4C2CBDB12DBA536D CRC64;

Query Match 43.8%; Score 7; DB 1; Length 433;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVGIGCT 7
 Db 383 LVGIGCT 389

RESULT 14
 ENOG_HUMAN
 ID ENOG_HUMAN STANDARD; PRT; 433 AA.
 AC P09104;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE GAMMA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
 DE (NEURAL ENOLASE) (NSE).
 GN ENO2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Retina;
 RX MEDLINE=89091176; PubMed=3208766;
 RA McLeese S.M., Dunbar B., Fothergill J., Hinks L., Day I.N.M.;
 RT "Complete amino acid sequence of the neurone-specific gamma isozyme
 of enolase (NSE) from human brain and comparison with the
 non-neuronal alpha form (NNE).";
 RL Eur. J. Biochem. 178:413-417(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9006764; PubMed=2792767;
 RA Oliva D., Barba G., Barbieri G., Giallongo A., Feo S.;
 RT "Cloning, expression and sequence homologies of cDNA for human gamma
 enolase";
 RL Gene 79:355-360(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Brain;
 RX MEDLINE=88259288; PubMed=3385803;
 RA van Obberghen E., Kamholz J., Bishop J.G. III, Zomzely-Neurath C.,
 RA Lazzerini R.A.;
 RT "Human gamma enolase: isolation of a cDNA clone and expression in
 normal and tumor tissues of human origin";
 RL J. Neurosci. Res. 19:450-456(1988).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Hematopoietic;
 RX MEDLINE=91257823; PubMed=2045099;
 RA Oliva D., Cali L., Feo S., Giallongo A.;
 RT "Complete structure of the human gene encoding neuron-specific
 enolase";
 RL Genomics 10:157-165(1991).
 RN [5]

Db		383	LVLGCT	389
	RESULT	15		
	ID	ENOG_MOUSE		
	ID	ENOG_MOUSE	STANDARD;	PRT; 433 AA.
		P17183;		
DT	01-AUG-1990	(Rel. 15, Created)		
DT	01-AUG-1990	(Rel. 15, Last sequence update)		
DT	15-JUL-1998	(Rel. 36, Last annotation update)		
DE	GAMMA ENOLASE [EC 4.2.1.11] (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)			
DE	(NEURAL ENOLASE) (NSE).			
OS	ENO2 OR ENO-2.			
OC	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=90301487; PubMed=2362815;			
RA	Kaghad M., Dumont X., Chalton P., Lelias J.M., Lamandé N., Lucas M.,			
RA	Lazar M., Caput D.;			
RT	"Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from			
RT	mouse brain."			
RL	Nucleic Acids Res. 18:3638-3658(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Ansaari-Lari M.A., Oeltjen J.C., Schwartz S., Zhang Z., Muzny D.M.,			
RA	Lu J., Gorrell J.H., Chinault A.C., Belmont J.W., Miller W.,			
RA	Gibbs R.A.;			
RL	Submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.			
CC	-1 CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSHOENOLPYRUVATE + H(2O).			
CC	-1 COPFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER.			
CC	-1 PATHWAY: GLYCOLYSIS.			
CC	-1 SUBUNIT: HOMODIMER.			
CC	-1 SUBCELLULAR LOCATION: CYTOPLASMIC.			
CC	-1 TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS FOUND ONLY IN NEUROUS TISSUE.			
CC	-1 SIMILARITY: BELONGS TO THE ENOLASE FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X52380; CAA36606.1; -			
DR	EMBL; AC002397; AAC36002.1; -			
DR	PIR; S10247; S10247.			
DR	HSSP; P56252; lPDY.			
DR	MGD; MG1:95394; Eno2.			
DR	InterPro: IPR000941; Enolase.			
DR	Pfam: PF00113; enolase: 1.			
DR	PRINTS; PR00148; ENOLASE.			
DR	ProDom; PD000902; Enolase; 1.			
DR	PROSITE; PS00164; ENOLASE; 1.			
KW	Lyase; Glycolysis; Magnesium; Multigene family.			
FT	INIT MET 0			
FT	ACT SITE 157 157			
FT	METAL 244 244			
FT	METAL 292 292			
FT	METAL 317 317			
SEQ	SEQUENCE 433 AA; 47165 MW; B7281132E637D43E CRC64;			

Query Match 43.88; Score 7; DB 1; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVVGLCT 7
|||||
DB 383 LVVGLCT 389

Search completed: May 8, 2002, 11:47:58
Job time: 98 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 8, 2002, 11:45:09 ; Search time 23.85 Seconds
(without alignments)
49.693 Million cell updates/sec

Title: US-09-647-457-2

Sequence: 1 LVYGLCTCQIKTGPAC 16

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 522463 seqs, 74073290 residues

Word size: 0

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

A.GeneSeq_1101:*

- 1: /SIDSR/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SIDSR/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SIDSR/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SIDSR/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SIDSR/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /SIDSR/gcgdata/geneseq/geneseq/AA1985.DAT:*
- 7: /SIDSR/gcgdata/geneseq/geneseq/AA1986.DAT:*
- 8: /SIDSR/gcgdata/geneseq/geneseq/AA1987.DAT:*
- 9: /SIDSR/gcgdata/geneseq/geneseq/AA1988.DAT:*
- 10: /SIDSR/gcgdata/geneseq/geneseq/AA1989.DAT:*
- 11: /SIDSR/gcgdata/geneseq/geneseq/AA1990.DAT:*
- 12: /SIDSR/gcgdata/geneseq/geneseq/AA1991.DAT:*
- 13: /SIDSR/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /SIDSR/gcgdata/geneseq/geneseq/AA1993.DAT:*
- 15: /SIDSR/gcgdata/geneseq/geneseq/AA1994.DAT:*
- 16: /SIDSR/gcgdata/geneseq/geneseq/AA1995.DAT:*
- 17: /SIDSR/gcgdata/geneseq/geneseq/AA1996.DAT:*
- 18: /SIDSR/gcgdata/geneseq/geneseq/AA1997.DAT:*
- 19: /SIDSR/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /SIDSR/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SIDSR/gcgdata/geneseq/geneseq/AA2000.DAT:*
- 22: /SIDSR/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	100.0	16	AAV43191	Schizophrenic deri
2	8	50.0	16	AAV43204	Schizophrenic deri
3	8	50.0	17	AAV43197	Schizophrenic deri
4	8	50.0	17	AAV43198	Schizophrenic deri
5	7	43.8	15	AAV43203	Schizophrenic deri
6	7	43.8	16	AAV43202	Schizophrenic deri
7	7	43.8	17	AAV43196	Schizophrenic deri
8	7	43.8	18	AAV43195	Schizophrenic deri
9	7	43.8	19	AAV43194	Schizophrenic deri
10	7	43.8	20	AAV43193	Schizophrenic deri
11	7	43.8	20	AAV43199	Schizophrenic deri

13	7	43.8	28	AAV43192	Schizophrenic deri
14	7	43.8	218	AAV43191	Breast and ovarian
15	7	43.8	429	AAV43197	Human ORFX ORF1828
16	7	43.8	433	AAV43198	Enolase protein.
17	6	37.5	19	AAV43200	Alpha Enolase. Ho
18	6	37.5	16	AAV43203	Schizophrenic deri
19	6	37.5	82	AAV43204	Human EST encoded
20	6	37.5	306	AAV43207	Moraxella catarrha
21	6	37.5	350	AAV43209	C glutamicum prote
22	6	37.5	350	AAV43210	Corynebacterium q1
23	6	37.5	2523	AAV43211	Human protein kina
24	5	31.2	7	AAV43212	Human microtubule
25	5	31.2	9	AAV43213	Uroplakin tumour a
26	5	31.2	12	AAV43214	Penicillin V amido
27	5	31.2	12	AAV43215	Schizophrenic deri
28	5	31.2	14	AAV43216	Cladosporium herba
29	5	31.2	16	AAV43217	Fibroblast growth
30	5	31.2	18	AAV43218	Antimicrobial cati
31	5	31.2	20	AAV43219	Bactolysin - antim
32	5	31.2	20	AAV43220	Cationic antimicro
33	5	31.2	21	AAV43221	Hepatitis GB virus
34	5	31.2	29	AAV43222	Staphylococcus aur
35	5	31.2	34	AAV43223	Human secreted pro
36	5	31.2	38	AAV43224	Human 5' EST seque
37	5	31.2	41	AAV43225	E21, monoclonal an
38	5	31.2	43	AAV43226	Human endometrium
39	5	31.2	66	AAV43227	Arabidopsis thalia
40	5	31.2	68	AAV43228	Plant SDF encoded
41	5	31.2	69	AAV43229	Secreted protein e
42	5	31.2	71	AAV43230	Amino acid sequenc
43	5	31.2	72	AAV43231	Human endometrium
44	5	31.2	74	AAV43232	Arabidopsis thalia
45	5	31.2	77	AAV43233	Human colon cancer

ALIGNMENTS

RESULT 1	AAV43191	standard; peptide; 16 AA.
ID	AAV43191	
XX	AAV43191	
AC	11-JAN-2000 (first entry)	
XX		
DE	Schizophrenic derived antibody binding epitope #1.	
XX	Schizophrenic derived antibody; binding epitope; schizophrenia;	
KW	platelet-associated antibody; diagnosis.	
OS	Synthetic.	
XX		
PN	W09951725-A2.	
XX		
PD	14-OCT-1999.	
XX		
PF	30-MAR-1999; 99WO-IL00190.	
XX		
PR	02-APR-1998; 98IL-0123925.	
XX		
PA	(YEDA) YEDA RES & DEV CO LTD.	
XX		
PI	Shinitzky M, Deckmann M;	
XX		
DR	WPI: 1999-611037/52.	
XX		
PT	New peptides useful for diagnosis of schizophrenia -	
XX		
PS	Claim.2; Page 21; 37pp; English.	
XX		
CC	This sequence is a peptide of the invention, which binds antibodies found	

Schizophrenic deri
Breast and ovarian
Human ORFX ORF1828
Enolase protein.
Alpha Enolase. Ho
Schizophrenic deri
Human EST encoded
Moraxella catarrha
C glutamicum prote
Corynebacterium q1
Human protein kina
Human microtubule
Uroplakin tumour a
Penicillin V amido
Schizophrenic deri
Cladosporium herba
Fibroblast growth
Antimicrobial cati
Bactolysin - antim
Cationic antimicro
Hepatitis GB virus
Staphylococcus aur
Human secreted pro
Human 5' EST seque
E21, monoclonal an
Human endometrium
Arabidopsis thalia
Plant SDF encoded
Secreted protein e
Amino acid sequenc
Human endometrium
Arabidopsis thalia
Human colon cancer

CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.

XX Sequence 16 AA;

Query Match 100.0%; Score 16; DB 20; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.8e-10;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCTCQIKTGPAC 16
 |||||
 DB 1 LVVGLCTCQIKTGPAC 16

RESULT 2

AA43204
 ID AAY43204 standard; peptide; 16 AA.

XX AAY43204;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #14.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
 platelet-associated antibody; diagnosis.

OS Synthetic.

PN WO951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL00190.

PR 02-APR-1998; 98IL-0123925.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

DE New peptides useful for diagnosis of schizophrenia -

PS Claim 4; Page 21; 37pp; English.

CC This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.

SO Sequence 16 AA;

Query Match

Best Local Similarity 50.0%; Score 8; DB 20; Length 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 QIKTGPAC 16
 |||||

DB 9 qiktgpac 16

RESULT 3

AA43197
 ID AAY43197 standard; peptide; 17 AA.

XX AAY43197;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #7.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
 platelet-associated antibody; diagnosis.

OS Synthetic.

PN WO951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL00190.

PR 02-APR-1998; 98IL-0123925.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

DE New peptides useful for diagnosis of schizophrenia -

PS Claim 3; Page 21; 37pp; English.

CC This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.

SO Sequence 17 AA;

Query Match

Best Local Similarity 50.0%; Score 8; DB 20; Length 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 QIKTGPAC 16
 |||||
 DB 9 qiktgpac 16

RESULT 4

AA43198
 ID AAY43198 standard; peptide; 17 AA.

XX AAY43198;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #8.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
 platelet-associated antibody; diagnosis.

OS Synthetic.

PN WO9951725-A2.
XX
PD 14-OCT-1999.
XX
PF 30-MAR-1999; 99WO-IL00190.
XX
PR 02-APR-1998; 98IL-0123925.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Shinitzky M, Deckmann M;
XX
DR WPI; 1999-611037/52.
XX
PT New peptides useful for diagnosis of schizophrenia -
XX
PS Claim 3; Page 21; 37pp; English.
XX
CC This sequence is a peptide of the invention, which binds antibodies found
CC in elevated levels in body fluids of schizophrenic patients. The peptide
CC is useful in an assay for the diagnosis of schizophrenia, by binding the
CC peptide to a platelet-containing fraction of blood, or a fraction
CC containing platelet-associated antibodies (PAA) shed from the platelets,
CC or preferably whole blood. The new peptides are able to differentiate
CC between plasma samples from schizophrenic and non-schizophrenic patients,
CC and can do so without having to first isolate the platelet-associated
CC antibodies (PAA) fraction.
XX
SQ Sequence 17 AA;

Query Match 50.0%; Score 8; DB 20; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 QIKTGPAC 16
| | | | | | | |
Db 9 qiktgpac 16

RESULT 5
AAV43203
ID AAV43203 standard; peptide; 15 AA.
XX
AC AAV43203;
XX
DT 11-JAN-2000 (first entry)
XX
DE Schizophrenic derived antibody binding epitope #13.
XX
KW Schizophrenic derived antibody; binding epitope; schizophrenia;
KW platelet-associated antibody; diagnosis.
XX
OS Synthetic.
XX
PN WO9951725-A2.
XX
PD 14-OCT-1999.
XX
PF 30-MAR-1999; 99WO-IL00190.
XX
PR 02-APR-1998; 98IL-0123925.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Shinitzky M, Deckmann M;
XX
DR WPI; 1999-611037/52.
XX
PT New peptides useful for diagnosis of schizophrenia -
XX
PS Claim 4; Page 21; 37pp; English.
XX

CC This sequence is a peptide of the invention, which binds antibodies found
CC in elevated levels in body fluids of schizophrenic patients. The peptide
CC is useful in an assay for the diagnosis of schizophrenia, by binding the
CC peptide to a platelet-containing fraction of blood, or a fraction
CC containing platelet-associated antibodies (PAA) shed from the platelets,
CC or preferably whole blood. The new peptides are able to differentiate
CC between plasma samples from schizophrenic and non-schizophrenic patients,
CC and can do so without having to first isolate the platelet-associated
CC antibodies (PAA) fraction.
XX
SQ Sequence 15 AA;

Query Match 43.8%; Score 7; DB 20; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVVGLCT 7
| | | | | | |
Db 1 lvvgllct 7

RESULT 6
AAV43202
ID AAV43202 standard; peptide; 16 AA.
XX
AC AAV43202;
XX
DT 11-JAN-2000 (first entry)
XX
DE Schizophrenic derived antibody binding epitope #12.
XX
KW Schizophrenic derived antibody; binding epitope; schizophrenia;
KW platelet-associated antibody; diagnosis.
XX
OS Synthetic.
XX
PN WO9951725-A2.
XX
PD 14-OCT-1999.
XX
PF 30-MAR-1999; 99WO-IL00190.
XX
PR 02-APR-1998; 98IL-0123925.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Shinitzky M, Deckmann M;
XX
DR WPI; 1999-611037/52.
XX
PT New peptides useful for diagnosis of schizophrenia -
XX
PS Claim 4; Page 21; 37pp; English.
XX
PN This sequence is a peptide of the invention, which binds antibodies found
CC in elevated levels in body fluids of schizophrenic patients. The peptide
CC is useful in an assay for the diagnosis of schizophrenia, by binding the
CC peptide to a platelet-containing fraction of blood, or a fraction
CC containing platelet-associated antibodies (PAA) shed from the platelets,
CC or preferably whole blood. The new peptides are able to differentiate
CC between plasma samples from schizophrenic and non-schizophrenic patients,
CC and can do so without having to first isolate the platelet-associated
CC antibodies (PAA) fraction.
XX
SQ Sequence 16 AA;

Query Match 43.8%; Score 7; DB 20; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVVGLCT 7

Db 1 LVVGLCT 7

RESULT 7

AAV43196 standard; peptide: 17 AA.

AC AAV43196;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #6.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
platelet-associated antibody; diagnosis.

OS Synthetic.

PN WO951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-1100190.

PR 02-APR-1998; 98IL-0123925.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

PT New peptides useful for diagnosis of schizophrenia -

PS Claim 3; Page 21; 37pp; English.

This sequence is a peptide of the invention, which binds antibodies found in elevated levels in body fluids of schizophrenic patients. The peptide is useful in an assay for the diagnosis of schizophrenia, by binding the peptide to a platelet-containing fraction of blood, or a fraction containing platelet-associated antibodies (PAA) shed from the platelets, or preferably whole blood. The new peptides are able to differentiate between plasma samples from schizophrenic and non-schizophrenic patients, and can do so without having to first isolate the platelet-associated antibodies (PAA) fraction.

SQ Sequence 17 AA;

Query Match 43.8%; Score 7; DB 20; Length 17;

Best Local Similarity 100.0%; Pred. No. 0.63; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7

Db 1 LVVGLCT 7

RESULT 8

AAV43195 standard; peptide: 18 AA.

AC AAV43195;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #5.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
platelet-associated antibody; diagnosis.

OS Synthetic.

XX WO951725-A2.

XX 14-OCT-1999.

XX 30-MAR-1999; 99WO-1100190.

XX 02-APR-1998; 98IL-0123925.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Shinitzky M, Deckmann M;

XX WPI; 1999-611037/52.

XX New peptides useful for diagnosis of schizophrenia -

XX Claim 3; Page 21; 37pp; English.

This sequence is a peptide of the invention, which binds antibodies found in elevated levels in body fluids of schizophrenic patients. The peptide is useful in an assay for the diagnosis of schizophrenia, by binding the peptide to a platelet-containing fraction of blood, or a fraction containing platelet-associated antibodies (PAA) shed from the platelets, or preferably whole blood. The new peptides are able to differentiate between plasma samples from schizophrenic and non-schizophrenic patients, and can do so without having to first isolate the platelet-associated antibodies (PAA) fraction.

SQ Sequence 18 AA;

Query Match 43.8%; Score 7; DB 20; Length 18;

Best Local Similarity 100.0%; Pred. No. 0.66; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7

Db 2 LVVGLCT 8

RESULT 9

AAV43194 standard; peptide: 19 AA.

AC AAV43194;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #4.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
platelet-associated antibody; diagnosis.

OS Synthetic.

PN WO951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-1100190.

PR 02-APR-1998; 98IL-0123925.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

PT New peptides useful for diagnosis of schizophrenia -

PS Claim 3; Page 21; 37pp; English.

XX This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.

XX Sequence 19 AA:

Query Match 43.8%; Score 7; DB 20; Length 19;
 Best Local Similarity 100.0%; Pred. No. 0.69;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
 |||||
 Db 3 lvvglt 9

RESULT 10

AAV43193
 ID AAV43193 standard; peptide; 20 AA.

XX AAV43193;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #3.

XX Schizophrenic derived antibody; binding epitope; schizophrenia;
 KW platelet-associated antibody; diagnosis.

XX Synthetic.

XX WO9951725-A2.

XX 14-OCT-1999.

PD 30-MAR-1999; 99WO-IL00190.

PF 02-APR-1998; 98IL-0123925.

PR (YEDA) YEDA RES & DEV CO LTD.

PA Shinitzky M, Deckmann M;

PI WPI; 1999-611037/52.

DR New peptides useful for diagnosis of schizophrenia -

PT Claim 3; Page 21; 37pp; English.

XX This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.

XX Sequence 20 AA:

Query Match 43.8%; Score 7; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.72;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
 |||||
 Db 4 lvvglt 10

RESULT 11

AAV43199
 ID AAV43199 standard; peptide; 20 AA.

XX AAV43199;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #9.

XX Schizophrenic derived antibody; binding epitope; schizophrenia;
 KW platelet-associated antibody; diagnosis.

XX Synthetic.

XX WO9951725-A2.

PN 14-OCT-1999.

PD 30-MAR-1999; 99WO-IL00190.

PF 02-APR-1998; 98IL-0123925.

PR (YEDA) YEDA RES & DEV CO LTD.

PA Shinitzky M, Deckmann M;

PI WPI; 1999-611037/52.

DR New peptides useful for diagnosis of schizophrenia -

PT Claim 4; Page 21; 37pp; English.

XX This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.

XX Sequence 20 AA:

Query Match 43.8%; Score 7; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.72;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
 |||||
 Db 12 lvvglt 18

RESULT 12

AAV43192
 ID AAV43192 standard; peptide; 28 AA.

XX AAV43192;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #2.

XX Schizophrenic derived antibody; binding epitope; schizophrenia;
 KW platelet-associated antibody; diagnosis.

OS Synthetic.
XX
XX WO951725-A2.
XX
XX 14-OCT-1999.
XX
XX 30-MAR-1999; 99WO-IL00190.
XX
XX 02-APR-1998; 98IL-0123925.
XX
XX (YEDA) YEDA RES & DEV CO LTD.
XX
XX Shinitzky M, Deckmann M;
XX
XX WPI; 1999-611037/52.
XX
XX New peptides useful for diagnosis of schizophrenia -
XX
XX Claim 3; Page 21; 37pp; English.
XX
XX This sequence is a peptide of the invention, which binds antibodies found
XX in elevated levels in body fluids of schizophrenic patients. The peptide
XX is useful in an assay for the diagnosis of schizophrenia, by binding the
XX peptide to a platelet-containing fraction of blood, or a fraction
XX containing platelet-associated antibodies (PAA) shed from the platelets,
XX or preferably whole blood. The new peptides are able to differentiate
XX between plasma samples from schizophrenic and non-schizophrenic patients,
XX and can do so without having to first isolate the platelet-associated
XX antibodies (PAA) fraction.
XX
XX Sequence 28 AA;
SQ

Query Match 43.8%; Score 7; DB 20; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVVGLCT 7
| | | | | | |
Db 12 LVVGLCT 18

RESULT 13
AAB58877
ID AAB58877 standard; Protein; 218 AA.
XX
XX AAB58877;
AC

DT 27-MAR-2001 (first entry)
XX

DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 585.
XX

KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW neutropenic; neuroprotective; antiviral; antifungal; hepatotropic;
KW antidiabetic; antiinflammatory; antitumor; vulnary; anticonvulsant;
KW antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
KW Addison's disease; allergy; autoimmune haemolytic anaemia;
KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW cardiovascular disorder; wound healing; neurological disease.
XX

OS Homo sapiens.
XX

PN WO20005173-A1.
XX

PD 21-SEP-2000.
XX

PF 08-MAR-2000; 2000WO-US05881.
XX

PR 12-MAR-1999; 99US-0124270.
XX

PA (HUMA-) HUMAN GENOME SCI INC.
XX

PI Rosen CA, Ruben SM;
XX
XX WPI; 2000-611515/58.
XX
XX N-PSDB; AAF21780.
XX
XX New human breast and ovarian cancer associated gene sequences and the
XX polypeptides encoded by these genes, useful in the prevention,
XX treatment and diagnosis of cancer, immune disorders, cardiovascular
XX disorders and neurological diseases -
XX
XX Claim 11; Page 1022-1023; 1299pp; English.
XX

XX Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
XX proteins AAB58711 - AAB59128. The DNA and protein sequences are
XX associated with breast and ovarian cancer. Included in the invention are
XX sequences AAF22032 - AAF22040 and AAB59129 which are used in the
XX isolation and characterisation of the DNA and protein sequences of the
XX invention. The breast and ovarian cancer associated DNA, protein, agonist
XX or antagonist sequences exhibit cytostatic; immunosuppressive;
XX neutropenic; neuroprotective; antiviral; antiallergic; hepatotropic;
XX antidiabetic; antiinflammatory; antitumor; vulnary; anticonvulsant;
XX antibacterial; antifungal; antiparasitic and cardiant activity. The
XX polynucleotide and protein sequences are used in the diagnosis of cancer,
XX particularly breast and ovarian cancer. The nucleic acid sequences,
XX proteins, agonists and antagonists may also be used in the diagnosis,
XX prevention and treatment of immune disorders e.g. Addison's disease,
XX allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
XX diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
XX arthritis and ulcerative colitis; cardiovascular disorders such as
XX myocardial ischaemia; wound healing; neurological diseases such as
XX cerebral anoxia and epilepsy; and infectious diseases.
XX

Sequence 218 AA;
SQ
Query Match 43.8%; Score 7; DB 21; Length 218;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVVGLCT 7
| | | | | | |
Db 43 LVVGLCT 49

RESULT 14
AAB42064
ID AAB42064 standard; Protein; 429 AA.
XX
XX AAB42064;
AC

DT 08-FEB-2001 (first entry)
XX

DE Human ORF1828 polypeptide sequence SEQ ID NO:3656.
XX

KW Human; open reading frame; ORF; detection; cytostatic; hepatotropic;
KW vulnary; antiparasitic; antiparasitoid; neutropenic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritis; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antineumatic; antithyroid;
KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antinflammatory disease; coagulation;
KW thrombosis; contraceptive.
XX

OS Homo sapiens.
XX

PN WO200058473-A2.
XX

PD 05-OCT-2000.
XX
PF 31-MAR-2000; 2000WO-US08621.
XX
PR 31-MAR-1999; 99US-0127607.
PR 02-APR-1999; 99US-0127636.
PR 05-APR-1999; 99US-0127728.
PR 30-MAR-2000; 2000US-0540763.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2000-602362/57.
DR N-PSDB; AAC76273.
XX
PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -
XX
PS Claim 11; Page 2810-2811; 5507pp; English.
XX
CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
CC antipariatic; antiparkinsonian; nootropic; neuroprotective;
CC osteoparatic; anticonvulsant; antithratic; immunosuppressant;
CC immunostimulant; cardiac; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatological; immunosuppressive;
CC antiinflammatory; antibacterial; antiviral; antifungal; antineumatic;
CC antihypertoid; and antianaemic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORFX-associated disorder. The
CC nucleic acids can be used to express ORFX proteins in gene therapy.
CC 'vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.
XX
SQ Sequence 429 AA;

Query Match 43.8%; Score 7; DB 21; Length 429;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
Db 379 LVVGLCT 385
|||||
|

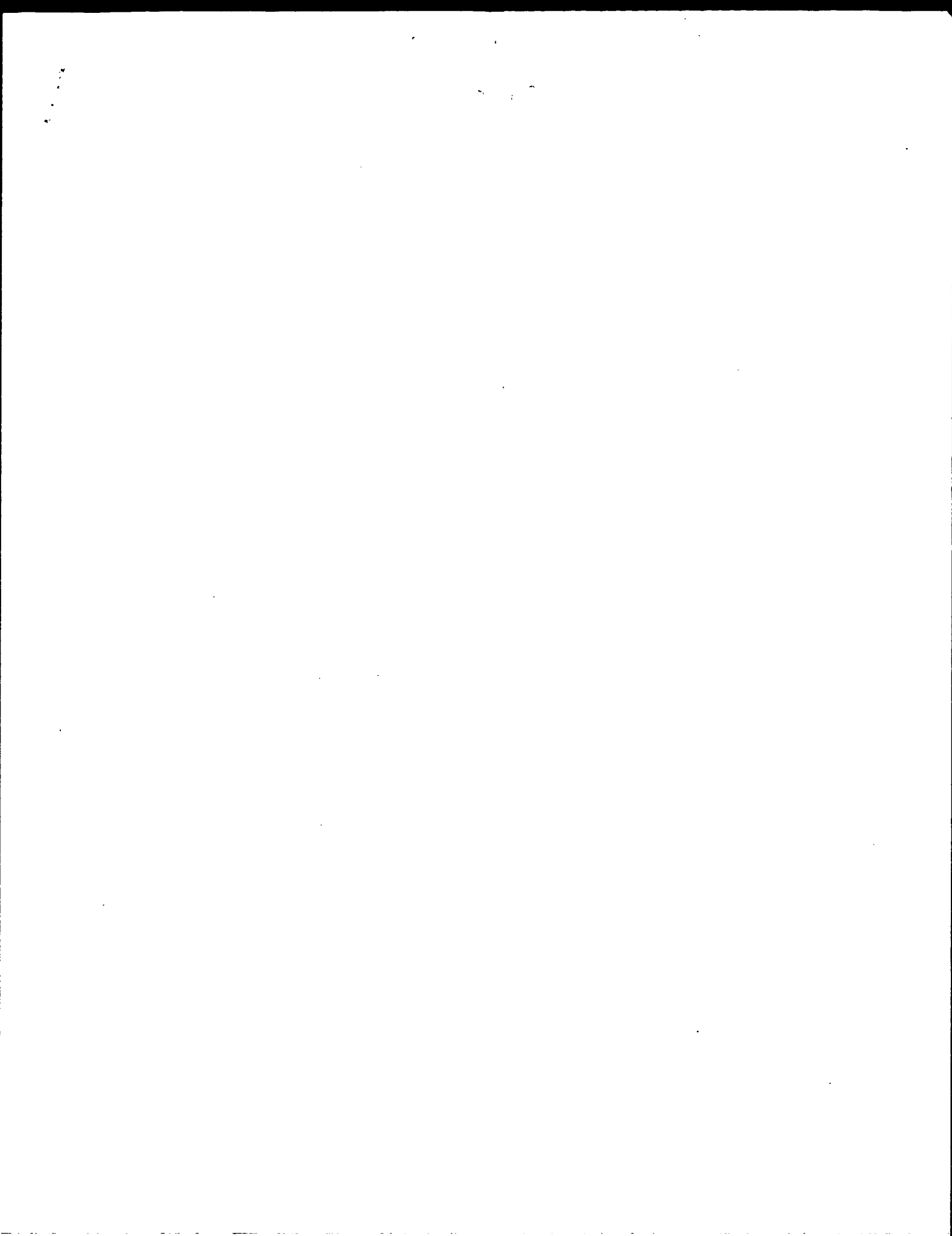
RESULT 15
AAW14001
ID AAW14001 standard; Protein; 433 AA.
XX
AC AAW14001;
XX
DT 23-MAY-1997 (first entry)
XX
DE Enolase protein.
XX
XX PCR; polymerase chain reaction; primer; amplify; tyrosine; human; NSE;
KW enolase; radioisotope; antigen.
XX
OS Homo sapiens.
XX
PN JF08308584-A.
XX

PD 26-NOV-1996.
XX
PF 19-MAY-1995; 95JP-0145542.
XX
PR 19-MAY-1995; 95JP-0145542.
XX
PA (EIKE) EIKEN KAGAKU KK.
XX
DR WPI; 1997-059703/06.
XX
PT Introducing tyrosine residues into a protein for radioisotopic
PT labelling - by substitution, addition and/or insertion to a DNA
PT coding for the protein, antigenicity of the protein is unchanged by
PT labelling
XX
PS Disclosure; Page 10-11; 13pp; Japanese.
XX
CC This sequence represents the wild type human enolase (NSE) protein. The
CC primers represented by AAT60282-T60285 were used to amplify tyrosine
CC introduced versions of this sequence. The introduced tyrosine residues
CC combine a radioisotope in such a way as to have no substantial effect on
CC the antigenicity of the protein. The peptides with the introduced
CC tyrosine residue are prepared by expressing a recombinant DNA sequence,
CC where the tyrosine residue has been introduced via an insertion or
CC substitution into the wild type sequence. The peptides can then be used
CC in radioimmunoassays, as the introduction of the label does not alter
CC the antigenicity of the protein.
XX
SQ Sequence 433 AA;

Query Match 43.8%; Score 7; DB 18; Length 433;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
Db 383 LVVGLCT 389
|||||
|

Search completed: May 8, 2002, 11:47:03
Job time: 114 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 8, 2002, 11:44:04 ; Search time 12.84 Seconds
(without alignments)
94.922 Million cell updates/sec

Title: US-09-647-457-2

Perfect score: 90

Sequence: 1 LVVGLCTCQIKTGPAC 16

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: PIR_68:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	82.2	458	2 I37360	phosphopyruvate hy
2	65	72.2	395	2 I50026	phosphopyruvate hy
3	65	72.2	433	2 A37210	phosphopyruvate hy
4	65	72.2	434	1 NOHUG	phosphopyruvate hy
5	65	72.2	434	1 NOMB	phosphopyruvate hy
6	65	72.2	434	1 NOXL	phosphopyruvate hy
7	65	72.2	434	2 A24742	phosphopyruvate hy
8	65	72.2	434	2 S10246	phosphopyruvate hy
9	65	72.2	434	2 S10247	phosphopyruvate hy
10	65	72.2	434	2 A29170	phosphopyruvate hy
11	65	72.2	434	2 A32132	phosphopyruvate hy
12	65	72.2	434	2 S02072	phosphopyruvate hy
13	65	72.2	434	2 S06756	phosphopyruvate hy
14	65	72.2	434	2 J04186	phosphopyruvate hy
15	65	72.2	434	2 J04187	phosphopyruvate hy
16	65	72.2	434	2 J04189	phosphopyruvate hy
17	65	72.2	434	2 A23126	phosphopyruvate hy
18	65	72.2	434	2 T25040	phosphopyruvate hy
19	65	72.2	434	2 A23850	phosphopyruvate hy
20	65	72.2	434	2 S07586	phosphopyruvate hy
21	65	72.2	434	2 A53655	phosphopyruvate hy
22	65	72.2	434	2 T03267	phosphopyruvate hy
23	65	72.2	434	2 J01186	phosphopyruvate hy
24	65	72.2	434	2 J01185	phosphopyruvate hy
25	65	72.2	434	2 J01187	phosphopyruvate hy
26	65	72.2	434	2 T02221	phosphopyruvate hy
27	65	72.2	434	2 S39203	phosphopyruvate hy
28	65	72.2	434	2 T12341	phosphopyruvate hy
29	65	72.2	434	2 S16257	phosphopyruvate hy

ALIGNMENTS

```

30      48      53.3      372 2 524996      phosphopyruvate hy
31      47.5      52.8      1620 2 T27283      hypothetical prote
32      47.5      52.8      2946 2 T15840      hypothetical prote
33      47      52.2      446 2 542206      phosphopyruvate hy
34      46.5      51.7      437 1 NOBY      phosphopyruvate hy
35      46.5      51.7      437 1 NOBY2      phosphopyruvate hy
36      46      51.1      125 1 VSWTA2      alpha-2-thionin -
37      46      51.1      137 2 S07648      thionin precursor,
38      46      51.1      477 2 B96768      protein enolase F2
39      44      48.9      43 2 S13581      collagen alpha 1(I
40      44      48.9      959 2 S48962      MSH1 protein - yea
41      43      47.8      85 2 E70531      hypothetical prote
42      43      47.8      456 2 S73562      phosphopyruvate hy
43      43      47.8      687 2 A49636      soluble vascular e
44      43      47.8      1006 2 T00050      hypothetical prote
45      43      47.8      1338 2 S09982      protein-tyrosine k

RESULT 1
I37360
phosphopyruvate hydratase (EC 4.2.1.11), lung - human
N:Alternate names: enolase
C:Species: Homo sapiens (man)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 22-Jun-1999
C:Accession: I37360; S22071
R:Verma, M.; Kuhl, R.N.
Biochem. Int. 30, 293-303, 1993
A:Title: Human lung enolase: cloning and sequencing of cDNA and its inducibility w
A:Reference number: I37360
A:Accession: I37360
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-458 <VER>
A:Cross-references: EMBL:X66610; NID:G31178; PIDN:CAA47179.1; PID:G31179
A:Note: submitted to the EMBL Data Library, June 1992
C:Function:
A:Description: catalyzes the reversible dehydration of 2-phospho-D-glycercic acid to
A:Pathway: gluconeogenesis; glycolysis
C:Superfamily: enolase
C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesiu
F:43/Binding site: magnesium 2 (Ser) #status predicted
F:219,364/Active site: Glu, Lys #status predicted
F:254,308,336/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match      82.2%      Score 74; DB 2; Length 458;
Best Local Similarity 87.5%; Pred.No. 0.00053;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGPAC 16
DB 407 LVVGLCTCQIKTGPAC 422

RESULT 2
I50026
phosphopyruvate hydratase (EC 4.2.1.11) alpha - American alligator (fragment)
N:Alternate names: alpha-enolase
C:Species: Alligator mississippiensis (American alligator)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 22-Jun-1999
C:Accession: I50026
R:Hedges, S.B.
Proc. Natl. Acad. Sci. U.S.A. 91, 2621-2624, 1994.
A:Title: Molecular evidence for the origin of birds.
A:Reference number: A53470; MUID:94195794
A:Accession: I50026
A>Status: preliminary; nucleic acid sequence not shown; translation not shown; tra
A:Molecule type: mRNA
A:Residues: 1-395 <HED>
A:Cross-references: GB:L28078; NID:G472796; PIDN:AA53671.1; PID:G472797

```

C:Superfamily: enolase
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 72.2%; Score 65; DB 2; Length 395;
Best Local Similarity 81.2%; Pred. No. 0.011;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
||||| |||||
Db 362 LVVGLCTGQIKTGAPC 377

RESULT 3
A37210
Phosphopyruvate hydratase (EC 4.2.1.11) beta - rabbit
N:Alternate names: enolase beta
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 05-Aug-1994
C:Accession: A37210
R:Chin, C.C.Q.
J. Protein Chem. 9, 427-432, 1990
A:Title: The primary structure of rabbit muscle enolase.
A:Reference number: A37210; MUID:9113295
A:Accession: A37210
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-433 <CHI>
C:Superfamily: enolase
C:Keywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase
F:1/Modified site: acetylated amino end (Ala) #status experimental

Query Match 72.2%; Score 65; DB 2; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
||||| |||||
Db 383 LVVGLCTGQIKTGAPC 398

RESULT 4
NOMHG
Phosphopyruvate hydratase (EC 4.2.1.11) gamma - human
N:Alternate names: enolase gamma; neuron-specific enolase
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 18-Jun-1999
C:Accession: J00060; S16163; S02077; I56569; S02616; S38303
R:Oliva, D.; Barba, G.; Bardieri, G.; Gallongo, A.; Feo, S.
Gene 79, 355-360, 1989
A:Title: Cloning, expression and sequence homologies of cDNA for human gamma enolase.
A:Reference number: J00060; MUID:90006764
A:Accession: J00060
A:Molecule type: mRNA
A:Residues: 1-434 <OLI>
A:Cross-references: GB:M22349; NID:9951199; PIDN:AAB59554.1; PID:g182116; GB:M27833
R:Oliva, D.; Call, L.; Feo, S.; Gallongo, A.
Genomics 10, 157-165, 1991
A:Title: Complete structure of the human gene encoding neuron-specific enolase.
A:Reference number: S16163; MUID:91257823
A:Accession: S16163
A:Molecule type: DNA
A:Residues: 1-434 <OLI>
A:Cross-references: GB:X51956; NID:g31164; PIDN:CAA36215.1; PID:g31165
R:McAleese, S.M.; Dunbar, B.; Fothergill, J.E.; Hinks, L.J.; Day, I.N.M.
Eur. J. Biochem. 178, 413-417, 1988
A:Title: Complete amino acid sequence of the neurone-specific gamma isozyme of enolase
A:Reference number: S02077; MUID:89091176
A:Accession: S02077
A:Molecule type: mRNA
A:Residues: 2-3, 'Q', 5-239, 'M', 241-434 <MCA>
A:Cross-references: EMBL:X13120; NID:g31145; PIDN:CAA31512.1; PID:g930063

A:Note: part of this sequence was confirmed by protein sequencing
A:Note: 264-Ala and 395-Ala were also found
R:Van Obberghen, E.; Kamholz, J.; Bishop, J.G.
J. Neurosci. Res. 19, 450-456, 1988
A:Title: Human gamma enolase: isolation of a cDNA clone and expression in normal rat
A:Reference number: I56569; MUID:88259288
A:Accession: I56569

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 'GC', 29-126, 'N', 128-434 <VAN>
A:Cross-references: GB:M36768; NID:g182117; PIDN:AAA5388.1; PID:g182118

R:Day, I.N.M.; Allsopp, M.T.E.P.; Moore, D.C.M.; Thompson, R.J.
FEBS Lett. 222, 139-143, 1987

A:Title: Sequence conservation in the 3'-untranslated regions of neurone-specific
A:Reference number: S02616; MUID:88005129
A:Accession: S02616

A:Status: not compared with conceptual translation
A:Molecule type: mRNA

A:Residues: 425-434 <DAY>
A:Cross-references: GB:Y00691; GB:M27610

R:Harrington, C.R.; Quinn, G.B.; Hurt, J.; Day, I.N.M.; Wischik, C.M.
Biochim. Biophys. Acta 1158, 120-128, 1993

A:Title: Characterisation of an epitope specific to the neuron-specific isoform of
of Delta/A4-protein.
A:Reference number: S38303; MUID:94002176
A:Accession: S38303

A:Molecule type: protein
A:Residues: 156-173 <HAR>

C:Comment: Enolase occurs with at least three isoforms (alpha, beta, and gamma) in
C:Comment: Thr-191 may be important for the enhanced tolerance to chloride ions of
C:Genetics:

A:Gene: GDB: ENO2

A:Cross-references: GDB:119872; OMIM:131360
A:Map position: 12p13-12p13

A:Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/2; 412/2
C:Complex: homodimer

C:Function:

A:Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to
A:Pathway: gluconeogenesis; glycolysis
C:Superfamily: enolase

F:2-434/Product: phosphopyruvate hydratase gamma #status predicted <MAT>
F:2/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #

F:210/Binding site: magnesium 2 (Ser) #status predicted
F:210/343/Active site: Glu, Lys #status predicted

F:245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 72.2%; Score 65; DB 1; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
||||| |||||
Db 384 LVVGLCTGQIKTGAPC 399

RESULT 5

NOMSB
Phosphopyruvate hydratase (EC 4.2.1.11) beta - mouse

N:Alternate names: enolase beta
C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 18-Jun-1999
C:Accession: S17109; S18036; S29675; A33921

R:Ramande, N.; Brosset, S.; Keller, A.; Lucas, M.; Lazar, M.
submitted to the EMBL Data Library, September 1991

A:Reference number: S17109
A:Accession: S17109

A:Molecule type: DNA
A:Residues: 1-434 <LAM>

A:Cross-references: EMBL:X61600; NID:g50848; PIDN:CAA43797.1; PID:g50849
R:Peterson, C.A.; Cho, M.; Rastinejad, F.; Blau, H.M.
submitted to the EMBL Data Library, October 1991

A:Description: Beta-enolase: a gene expressed in undifferentiated postnatal myoblasts th
A:Reference number: S18036
A:Accession: S18036
A:Molecule type: mRNA
A:Residues: 1-434 <PEP>
A:Cross-references: EMBL:X62667; NID:g50143; PIDN:CAA44540.1; PID:g50144
R:Lazar, M.; Lamande, N.; Brosset, S.; Lucas, M.; Keller, A.
submitted to the EMBL Data Library, February 1991
A:Reference number: S29675
A:Accession: S29675
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-434 <LA2>
A:Cross-references: EMBL:X57747; NID:g50846; PIDN:CAA40913.1; PID:g50847
R:Lamande, N.; Mazo, A.M.; Lucas, M.; Montarras, D.; Pinset, C.; Gros, F.; Legault-Demar
Proc. Natl. Acad. Sci. U.S.A. 86, 4445-4449, 1989
A:Title: Murine muscle-specific enolase: cDNA cloning, sequence, and developmental expre
A:Reference number: A33921; MUID:89282789
A:Accession: A33921
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 59-233, 'NA', 236-434 <LA2>
A:Cross-references: GB:M20745; NID:g193029; PIDN:AAA37554.1; PID:g387144
A:Experimental source: skeletal muscle
A:Genetics:
A:Insertions: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2
A:Function:
A:Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phos
A:Pathway: gluconeogenesis; glycolysis
A:Superfamily: enolase
C:Keywords: carbon-carbon lyase; carbon-oxygen lyase; dimer; gluconeogenesis; glycolysis
F:40/Binding site: magnesium 2 (Ser) #status predicted
F:210,343/Active site: Glu, Lys #status predicted
F:245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 72.2%; Score 65; DB 1; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
DB 384 LVVGLCTGQIKTGAPC 399

RESULT 6
NOXI
phosphopyruvate hydratase (EC 4.2.1.11) ENOI - African clawed frog
N:Alternate names: enolase ENOI
C:Species: Xenopus laevis (African clawed frog)
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 18-Jun-1999
C:Accession: S00463
R:Segall, N.; Shrutkowski, A.; Dworkin, M.B.; Dworkin-Rastl, E.
Biochem. J. 251, 31-39, 1988
A:Title: Enolase isoenzymes in adult and developing Xenopus laevis and characterization
A:Reference number: S00463; MUID:88268812
A:Accession: S00463
A:Molecule type: mRNA
A:Residues: 1-434 <SEG>
A:Cross-references: EMBL:Y00718; NID:g64679; PIDN:CAA68706.1; PID:g64680
C:Genetics:
A:Gene: ENOI
C:Function:
A:Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phos
A:Pathway: gluconeogenesis; glycolysis
C:Superfamily: enolase
C:Keywords: carbon-oxygen lyase; dimer; gluconeogenesis; glycolysis; hydro-lyase; magnes
F:40/Binding site: magnesium 2 (Ser) #status predicted
F:210,343/Active site: Glu, Lys #status predicted
F:245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 72.2%; Score 65; DB 1; Length 434;

Best Local Similarity 81.2%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
DB 384 LVVGLCTGQIKTGAPC 399

RESULT 7
A24742
phosphopyruvate hydratase (EC 4.2.1.11) gamma - rat
N:Alternate names: 2-phospho-glycerate dehydratase; enolase gamma; neuronal enolase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 22-Jun-1999
C:Accession: A24742; PQ0006
R:Sakimura, K.; Kushiya, E.; Obinata, M.; Odani, S.; Takahashi, Y.
Proc. Natl. Acad. Sci. U.S.A. 82, 7453-7457, 1985
A:Title: Molecular cloning and the nucleotide sequence of cDNA for neuron-specific
A:Reference number: A24742; MUID:86042683
A:Accession: A24742
A:Molecule type: mRNA
A:Residues: 1-434 <SAK>
A:Cross-references: GB:M11931; NID:g204041; PIDN:AAA41119.1; PID:g204042
R:Sakimura, K.; Kushiya, E.; Takahashi, Y.; Suzuki, Y.
Gene 60, 103-113, 1987
A:Title: The structure and expression of neuron-specific enolase gene.
A:Reference number: PQ0006; MUID:88152493
A:Accession: PQ0006
A:Molecule type: DNA
A:Residues: 1-28 <SA2>
A:Cross-references: GB:M22770; GB:M18742; NID:g205766; PIDN:AAA41725.1; PID:g554480
C:Superfamily: enolase
C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match 72.2%; Score 65; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
DB 384 LVVGLCTGQIKTGAPC 399

RESULT 8
S10246
phosphopyruvate hydratase (EC 4.2.1.11) alpha - mouse
N:Alternate names: 2-phosphoglycerate dehydratase; enolase alpha
C:Species: Mus musculus (house mouse)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 22-Jun-1999
C:Accession: S10246; A56781
R:Knapth, M.; Dumont, X.; Chalon, P.; Lelias, J.M.; Lamande, N.; Lucas, M.; Lazar,
Nucleic Acids Res. 18, 3638, 1990
A:Title: Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from mouse brain
A:Reference number: S10246; MUID:90301487
A:Accession: S10246
A:Molecule type: mRNA
A:Residues: 1-434 <KAG>
A:Cross-references: EMBL:X52379; NID:g55490; PIDN:CAA36605.1; PID:g55491
R:Botallico, L.A.; Kendrick, N.C.; Keller, A.; Li, Y.; Tabas, I.
Arterioscler. Thromb. 13, 264-275, 1993
A:Title: Cholesteryl ester loading of mouse peritoneal macrophages is associated with
soform.
A:Reference number: A56781; MUID:93152553
A:Accession: A56781
A>Status: preliminary
A:Molecule type: protein
A:Residues: 'X', 60, 'X', 62-67, 'X', 69-71, 'XX', 100-109, 'X', 111-112, 'X', 114, 'X', 184-187
A:Experimental source: peritoneal macrophages
A>Note: sequence modified after extraction from NCBI backbone
C:Superfamily: enolase
C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match 72.2% Score 65; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
||||| |||||
Db 384 LVVGLCTGQIKTGAPC 399

RESULT 9

S10247

phosphopyruvate hydratase (EC 4.2.1.11) gamma - mouse

N:Alternate names: 2-phosphoglycerate dehydratase; enolase gamma

C:Species: Mus musculus (house mouse)

C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 22-Jun-1999

C:Accession: S10247

R:Kaghad, M.; Dumont, X.; Chalou, P.; Lellias, J.M.; Lamande, N.; Lucas, M.; Lazar, M.; C

Nucleic Acids Res 18, 3638, 1990

A:Title: Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from mouse brain.

A:Reference number: S10246; MUID:90301487

A:Accession: S10247

A:Molecule type: mRNA

A:Residues: 1-434 <KAG>

A:Cross-references: EMBL:X52380; NID:955494; PIDN:CAA36606.1; PID:955495

C:Superfamily: enolase

C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match

Best Local Similarity 72.2% Score 65; DB 2; Length 434;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
||||| |||||
Db 384 LVVGLCTGQIKTGAPC 399

RESULT 10

A29170

phosphopyruvate hydratase (EC 4.2.1.11) alpha - human

N:Alternate names: 2-phosphoglycerate dehydratase; enolase 1; enolase alpha

C:Species: Homo sapiens (man)

C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Jun-2000

C:Accession: S11696; A29170; S52858; A39183

R:Giallongo, A.; Oliva, D.; Calli, L.; Barba, G.; Barbieri, G.; Feo, S.

Eur. J. Biochem. 190, 567-573, 1990

A:Title: Structure of the human gene for alpha-enolase.

A:Reference number: S11696; MUID:90323004

A:Accession: S11696

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-434 <GIA>

A:Cross-references: EMBL:X16288; NID:931172; PIDN:CAA34360.1; PID:91167843

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1989

R:Giallongo, A.; Feo, S.; Moore, R.; Croce, C.M.; Shown, L.C.

Proc. Natl. Acad. Sci. U.S.A. 83, 6741-6745, 1986

A:Title: Molecular cloning and nucleotide sequence of a full-length cDNA for human alpha

A:Reference number: A29170; MUID:86313654

A:Accession: A29170

A:Molecule type: mRNA

A:Residues: 1-434 <G12>

A:Cross-references: GB:M4328; NID:9182113; PIDN:AAA5387.1; PID:9182114

A:Note: the authors translated the codon AAG for residue 193 as His

R:Walter, M.; Laidenberger, F.A.; Schweppe, K.W.; Berg, H.; Northmann, W.

submitted to the EMBL Data Library, February 1995

A:Description: Autoreactive epitopes within the human alpha-enolase and their recognition

A:Reference number: S52858

A:Accession: S52858

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-251, 'S', 253-434 <NAL>

A:Cross-references: EMBL:X84907; NID:9693932; PIDN:CAA59331.1; PID:9693933

A:Experimental source: endometrium carcinoma cell line HEC-1B
R:Milnes, L.A.; Dahlberg, C.M.; Plescia, J.; Fellez, J.; Kato, K.; Plov, E.F.
Biochemistry 30, 1682-1691, 1991

A:Title: Role of cell-surface lysines in plasminogen binding to cells: identification

A:Reference number: A39183; MUID:91129243

A:Accession: A39183

A:Molecule type: protein

A:Residues: 170-182, 'I', 184, 'R', 186-190, 245-252 <MLT>

C:Genetics:

A:Gene: GDB:ENO1

A:Cross-references: GDB:119871; OMIM:172430

A:Map position: 1p36-1p36

A:Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2

C:Function:

A:Description: catalyzes the reversible hydration of phosphoenolpyruvate to 2-phosph

C:Superfamily: enolase

C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesiu

F:2-434/Product: phosphopyruvate hydratase alpha #status predicted <MAN>

Query Match 72.2% Score 65; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
||||| |||||
Db 384 LVVGLCTGQIKTGAPC 399

RESULT 11

A32132

phosphopyruvate hydratase (EC 4.2.1.11) alpha - duck

N:Alternate names: enolase alpha; tau-crystallin

C:Species: Anas platyrhynchos (domestic duck)

C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 21-Jun-2000

C:Accession: A32132

R:Wistow, G.J.; Lietman, T.; Williams, L.A.; Stapel, S.O.; de Jong, W.W.; Horwitz, J.

J. Cell Biol. 107, 2729-2736, 1988

A:Title: Tau-crystallin/alpha-enolase: one gene encodes both an enzyme and a lens s

A:Reference number: A92750; MUID:89079778

A:Accession: A32132

A:Molecule type: mRNA

A:Residues: 1-434 <WIS>

A:Cross-references: GB:X14195; NID:962455; PIDN:CAA32409.1; PID:962456

C:Superfamily: enolase

C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match 72.2% Score 65; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
||||| |||||
Db 384 LVVGLCTGQIKTGAPC 399

RESULT 12

S02072

phosphopyruvate hydratase (EC 4.2.1.11) beta - rat

N:Alternate names: enolase beta; enolase, muscle-specific

C:Species: Rattus norvegicus (Norway rat)

C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 22-Jun-1999

C:Accession: S02072

R:Ohshima, Y.; Mitsui, H.; Takayama, Y.; Kushiya, E.; Sakimura, K.; Takahashi, Y.

FEBS Lett. 242, 425-430, 1989

A:Title: cDNA cloning and nucleotide sequence of rat muscle-specific enolase (beta-p

A:Reference number: S02072; MUID:89121113

A:Accession: S02072

A:Molecule type: mRNA

A:Residues: 1-434 <OHS>

A:Cross-references: EMBL:X00979; NID:957781; PIDN:CAA68788.1; PID:957782

A:Note: the sequence from Fig. 4 is inconsistent with that from Fig. 2 in having 40.

C:Superfamily: enolase
C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; muscle

Query Match 72.2%; Score 65; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
|||||
DB 384 LVVGLCTGQIKTGAPC 399

RESULT 13

S06756

phosphopyruvate hydratase (EC 4.2.1.11) beta - human

N:Alternate names: enolase beta; enolase, skeletal muscle; phosphopyruvate hydratase, mu
C:Species: Homo sapiens (man)

C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 22-Jun-1999

C:Accession: S06756; S14759; S15933; S33330; S08685; S31650

R:Peshavaria, M.; Hinks, L.J.; Day, I.N.M.
Nucleic Acids Res. 17, 8862, 1989

A:Title: Structure of human muscle (beta) enolase mRNA and protein deduced from a genomic
A:Reference number: S06756; MUID:90067857

A:Accession: S06756
A:Molecule type: mRNA

A:Residues: 1-434 <PE>
A:Cross-references: EMBL:X16504; NID:g31169; PIDN:CAA34513.1; PID:g31170

R:Peshavaria, M.; Day, I.N.M.
Biochem. J. 275, 427-433, 1991

A:Title: Molecular structure of the human muscle-specific enolase gene (ENOS).
A:Reference number: S14759; MUID:91222137

A:Accession: S14759
A:Status: nucleic acid sequence not shown

A:Molecule type: DNA
A:Residues: 1-434 <PE2>

A:Cross-references: EMBL:X55976
R:Call, L.; Feo, S.; Oliva, D.; Gallongo, A.

Nucleic Acids Res. 18, 1893, 1990

A:Title: Nucleotide sequence of a cDNA encoding the human muscle-specific enolase (MSE).
A:Reference number: S15933; MUID:90245587

A:Accession: S15933
A:Molecule type: mRNA

A:Residues: 1-84, 'A', 86-161, 'K', 163-434 <CAL>
A:Cross-references: EMBL:X51957; NID:g34788; PIDN:CAA36216.1; PID:g34789

R:Gallongo, A.; Venturilla, S.; Oliva, D.; Bardieri, G.; Rubino, P.; Feo, S.
Eur. J. Biochem. 214, 367-374, 1993

A:Title: Structural features of the human gene for muscle-specific enolase. Differential
A:Reference number: S33330; MUID:93292497

A:Accession: S33330
A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-161, 'K', 163-434 <GIA>

A:Cross-references: EMBL:X56832; NID:g31166; PIDN:CAA40163.1; PID:g31167
A:Note: The nucleotide sequence was submitted to the EMBL Data Library, November 1990

C:Genetics:
A:Gene: GDB:ENOS

A:Cross-references: GDB:119873; OMIM:131370
A:Map position: 17pter-17p12

A:Insertions: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2
C:Superfamily: enolase

C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; muscle; skele

Query Match 72.2%; Score 65; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
|||||
DB 384 LVVGLCTGQIKTGAPC 399

RESULT 14

JC4186

phosphopyruvate hydratase (EC 4.2.1.11) alpha chain - chicken

N:Alternate names: alpha-2-phospho-D-glycerate hydrolase; enolase
C:Species: Gallus gallus (chicken)

C>Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000

C:Accession: JC4186
R:Tanaka, M.; Maeda, K.; Nakashima, K.

J. Biochem. 117, 554-559, 1995
A:Title: Chicken alpha-enolase but not beta-enolase has a Src-dependent tyrosine-p

A:Reference number: JC4186; MUID:95353505
A:Accession: JC4186

A:Molecule type: mRNA
A:Residues: 1-434 <TRAN>

A:Cross-references: DDBJ:D37900; NID:g974175; PIDN:BA07132.1; PID:g974176
A:Experimental source: Brain

C:Comment: This is a glycolytic enzyme and multiple isoenzyme forms were reported
rates for tyrosine phosphorylation in Rous sarcoma virus and is important in all t

C:Superfamily: enolase
C:Keywords: carbon-oxygen lyase; hydro-lyase; phosphoprotein

F/44/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 72.2%; Score 65; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
|||||
DB 384 LVVGLCTGQIKTGAPC 399

RESULT 15

JC4187

phosphopyruvate hydratase (EC 4.2.1.11) beta chain - chicken

N:Alternate names: beta-2-phospho-D-glycerate hydrolase; enolase
C:Species: Gallus gallus (chicken)

C>Date: 14-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000

C:Accession: JC4187
R:Tanaka, M.; Maeda, K.; Nakashima, K.

J. Biochem. 117, 554-559, 1995
A:Title: Chicken alpha-enolase but not beta-enolase has a Src-dependent tyrosine-p

A:Reference number: JC4186; MUID:95353505
A:Accession: JC4187

A:Molecule type: mRNA
A:Residues: 1-434 <TRAN>

A:Cross-references: DDBJ:D37901; NID:g974177; PIDN:BA07133.1; PID:g1616990
C:Comment: This is a glycolytic enzyme and multiple isoenzyme forms were reported

rates for tyrosine phosphorylation in Rous sarcoma virus and is important in all t
C:Superfamily: enolase

C:Keywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase; phosphoprotein
F/1/Modified site: acetylated amino end (Met) #status experimental

Query Match 72.2%; Score 65; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
|||||
DB 384 LVVGLCTGQIKTGAPC 399

Search completed: May 8, 2002, 11:45:46
Job time: 102 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 8, 2002, 11:41:39 ; Search time 23.95 Seconds
(Without alignments)
49,485 Million cell updates/sec

Title: US-09-647-457-2
Perfect score: 90
Sequence: 1 LVVGLCTCQIKTGPAC 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

A.Geneseq_1101:*

- 1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT:*
- 7: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT:*
- 8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT:*
- 9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT:*
- 10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT:*
- 11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT:*
- 12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT:*
- 13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT:*
- 15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT:*
- 16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT:*
- 17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT:*
- 18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT:*
- 19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT:*
- 22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	90	100.0	16	20	AAV43191	Schizophrenic deri
2	78	86.7	16	20	AAV43204	Schizophrenic deri
3	78	86.7	17	20	AAV43197	Schizophrenic deri
4	78	86.7	17	20	AAV43198	Schizophrenic deri
5	65	72.2	16	20	AAV43202	Schizophrenic deri
6	65	72.2	17	20	AAV43196	Schizophrenic deri
7	65	72.2	18	20	AAV43195	Schizophrenic deri
8	65	72.2	19	20	AAV43194	Schizophrenic deri
9	65	72.2	20	20	AAV43193	Schizophrenic deri
10	65	72.2	28	20	AAV43192	Schizophrenic deri
11	65	72.2	429	21	AAV42064	Human OREF ORF1828

12	65	72.2	433	18	AAV14001	
13	65	72.2	433	19	AAV54357	
14	61	67.8	16	20	AAV43200	
15	58	64.4	15	20	AAV43203	
16	51	56.7	68	21	AAV20166	
17	51	56.7	77	21	AAV20165	
18	51	56.7	78	21	AAV20164	
19	51	56.7	352	21	AAV37553	
20	51	56.7	444	21	AAV37552	
21	51	56.7	469	21	AAV37551	
22	46	51.1	45	2	AAV10126	
23	46	51.1	45	12	AAV10420	
24	46	51.1	45	12	AAV12496	
25	46	51.1	46	19	AAV66467	
26	46	51.1	46	21	AAV97565	
27	44	48.9	286	22	AAV14627	
28	44	48.9	959	16	AAV6066	
29	44	48.9	971	16	AAV6070	
30	43	47.8	12	20	AAV43201	
31	43	47.8	452	22	AAV97591	
32	43	47.8	462	22	AAV97592	
33	43	47.8	557	22	AAV97590	
34	43	47.8	567	22	AAV97593	
35	43	47.8	567	22	AAV97597	
36	43	47.8	661	20	AAV68009	
37	43	47.8	687	15	AAV62485	
38	43	47.8	687	19	AAV44841	
39	43	47.8	687	19	AAV47036	
40	43	47.8	687	20	AAV68005	
41	43	47.8	758	18	AAV36138	
42	43	47.8	758	18	AAV13395	
43	43	47.8	780	15	AAV62487	
44	43	47.8	780	19	AAV47039	
45	43	47.8	780	20	AAV68008	

ALIGNMENTS

RESULT 1
AAV43191 standard; peptide; 16 AA.
ID AAV43191
XX AAV43191;
XX
DT 11-JAN-2000 (first entry)
XX
XX Schizophrenic derived antibody binding epitope #1.
DE Schizophrenic derived antibody; binding epitope; schizophrenia;
KW platelet-associated antibody; diagnosis.
XX
XX Synthetic.
OS
XX
XX W09951725-A2.
PN
XX
XX 14-OCT-1999.
PD
XX
XX 30-MAR-1999; 99WO-IL00190.
PF
XX
XX 02-APR-1998; 98IL-0123925.
PR
XX
XX (YEDA) YEDA RES & DEV CO LTD.
PA
XX
XX Shinitzky M, Deckmann M;
PI
XX
XX WPI; 1999-611037/52.
DR
XX
XX New peptides useful for diagnosis of schizophrenia -
PT
XX
XX Claim 2; Page 21; 37pp; English.
PS
XX
XX This sequence is a peptide of the invention, which binds antibodies found

Pos

* Enolase protein.
* Alpha Enolase. Ho
Schizophrenic deri
Schizophrenic deri
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Sequence of antitu
Anticancer compsn.
Alphal-purothionin
Cationic peptide t
Cationic peptide t
Novel bone marrow
Yeast MSH1 protein
Yeast MSH1 protein
Schizophrenic deri
Fli1 receptor fusi
Fli1 receptor fusi
Fli1 receptor fusi
Fli1 receptor fusi
Human soluble vasc
Human SVGF-R1. H
Human soluble VEGF
Soluble VEGF recep
Human soluble vasc
Human VEGF recepto
Amino-terminal fra
Truncated Fli1 SVGF
Soluble truncated
Human soluble vasc

CC in elevated levels in body fluids of schizophrenic patients. The peptide
CC is useful in an assay for the diagnosis of schizophrenia, by binding the
CC peptide to a platelet-containing fraction of blood, or a fraction
CC containing platelet-associated antibodies (PAA) shed from the platelets,
CC or preferably whole blood. The new peptides are able to differentiate
CC between plasma samples from schizophrenic and non-schizophrenic patients,
CC and can do so without having to first isolate the platelet-associated
CC antibodies (PAA) fraction.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 90; DB 20; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGPAC 16
DB 1 LVVGLCTGQIKTGPAC 16

RESULT 2

AAV43204
ID AAV43204 standard; peptide: 16 AA.

XX
AC AAV43204;

DT 11-JAN-2000 (first entry)

XX Schizophrenic derived antibody binding epitope #14.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
XX platelet-associated antibody; diagnosis.

OS Synthetic.

PN WO9951725-A2.

XX 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL00190.

PR 02-APR-1998; 98IL-0123925.

XX (YEDA) YEDA RES & DEV CO LTD.

PA Shinitzky M, Deckmann M;

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

XX New peptides useful for diagnosis of schizophrenia -

PT Claim 4; Page 21; 37pp; English.

PS This sequence is a peptide of the invention, which binds antibodies found
CC in elevated levels in body fluids of schizophrenic patients. The peptide
CC is useful in an assay for the diagnosis of schizophrenia, by binding the
CC peptide to a platelet-containing fraction of blood, or a fraction
CC containing platelet-associated antibodies (PAA) shed from the platelets,
CC or preferably whole blood. The new peptides are able to differentiate
CC between plasma samples from schizophrenic and non-schizophrenic patients,
CC and can do so without having to first isolate the platelet-associated
CC antibodies (PAA) fraction.
XX
SQ Sequence 16 AA;

Query Match 86.7%; Score 78; DB 20; Length 16;
Best Local Similarity 93.8%; Pred. No. 0.00021;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGPAC 16
DB 1 LVVGLCTGQIKTGPAC 16

DB 1 LVVGLCTGQIKTGPAC 16

RESULT 3

AAV43197
ID AAV43197 standard; peptide: 17 AA.

XX
AC AAV43197;

DT 11-JAN-2000 (first entry)

XX Schizophrenic derived antibody binding epitope #7.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
XX platelet-associated antibody; diagnosis.

OS Synthetic.

PN WO9951725-A2.

XX 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL00190.

PR 02-APR-1998; 98IL-0123925.

XX (YEDA) YEDA RES & DEV CO LTD.

PA Shinitzky M, Deckmann M;

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

XX New peptides useful for diagnosis of schizophrenia -

PT Claim 3; Page 21; 37pp; English.

PS This sequence is a peptide of the invention, which binds antibodies found
CC in elevated levels in body fluids of schizophrenic patients. The peptide
CC is useful in an assay for the diagnosis of schizophrenia, by binding the
CC peptide to a platelet-containing fraction of blood, or a fraction
CC containing platelet-associated antibodies (PAA) shed from the platelets,
CC or preferably whole blood. The new peptides are able to differentiate
CC between plasma samples from schizophrenic and non-schizophrenic patients,
CC and can do so without having to first isolate the platelet-associated
CC antibodies (PAA) fraction.
XX
SQ Sequence 17 AA;

Query Match 86.7%; Score 78; DB 20; Length 17;
Best Local Similarity 93.8%; Pred. No. 0.00021;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGPAC 16
DB 1 LVVGLCTGQIKTGPAC 16

RESULT 4

AAV43198
ID AAV43198 standard; peptide: 17 AA.

XX
AC AAV43198;

DT 11-JAN-2000 (first entry)

XX Schizophrenic derived antibody binding epitope #8.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
XX platelet-associated antibody; diagnosis.

OS Synthetic.

PN WO9951725-A2.
 XX 14-OCT-1999.
 PD 30-MAR-1999; 99WO-IL00190.
 PF 02-APR-1998; 98IL-0123925.
 PR (YEDA) YEDA RES & DEV CO LTD.
 XX Shinitzky M, Deckmann M;
 XX WPI; 1999-611037/52.
 DR WPI; 1999-611037/52.
 XX New peptides useful for diagnosis of schizophrenia -
 PT Claim 3; Page 21; 37pp; English.
 PS This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.
 CC Sequence 17 AA;
 SQ

Query Match 86.7%; Score 78; DB 20; Length 17;
 Best Local Similarity 93.8%; Pred. No. 0.00021;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGPAC 16
 |||||
 Db 1 LVVGLCTPQIKTGPAC 16

RESULT 5
 AAY43202
 ID AAY43202 standard; peptide; 16 AA.
 XX
 AC AAY43202;
 XX
 DT 11-JAN-2000 (first entry)
 DE Schizophrenic derived antibody binding epitope #12.
 XX Schizophrenic derived antibody; binding epitope; schizophrenia;
 KW platelet-associated antibody; diagnosis.
 XX Synthetic.
 OS
 XX WO9951725-A2.
 PN 14-OCT-1999.
 PD 30-MAR-1999; 99WO-IL00190.
 PF 02-APR-1998; 98IL-0123925.
 PR (YEDA) YEDA RES & DEV CO LTD.
 XX Shinitzky M, Deckmann M;
 XX WPI; 1999-611037/52.
 DR WPI; 1999-611037/52.
 XX New peptides useful for diagnosis of schizophrenia -
 PT Claim 4; Page 21; 37pp; English.
 PS
 XX

CC This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.
 CC Sequence 16 AA;
 SQ

Query Match 72.2%; Score 65; DB 20; Length 16;
 Best Local Similarity 81.2%; Pred. No. 0.012;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGPAC 16
 |||||
 Db 1 LVVGLCTPQIKTGPAC 16

RESULT 6
 AAY43196
 ID AAY43196 standard; peptide; 17 AA.
 XX
 AC AAY43196;
 XX
 DT 11-JAN-2000 (first entry)
 DE Schizophrenic derived antibody binding epitope #6.
 XX Schizophrenic derived antibody; binding epitope; schizophrenia;
 KW platelet-associated antibody; diagnosis.
 XX Synthetic.
 OS
 XX WO9951725-A2.
 PN 14-OCT-1999.
 PD 30-MAR-1999; 99WO-IL00190.
 PF 02-APR-1998; 98IL-0123925.
 PR (YEDA) YEDA RES & DEV CO LTD.
 XX Shinitzky M, Deckmann M;
 XX WPI; 1999-611037/52.
 DR WPI; 1999-611037/52.
 XX New peptides useful for diagnosis of schizophrenia -
 PT Claim 3; Page 21; 37pp; English.
 PS
 XX

CC This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.
 CC Sequence 17 AA;
 SQ

Query Match 72.2%; Score 65; DB 20; Length 17;
 Best Local Similarity 81.2%; Pred. No. 0.013;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGPAC 16

Db 1 lvvgictgqiktgapc 16

RESULT 7

ID AAY43195 standard; peptide: 18 AA.

AC AAY43195;

DT 11-JAN-2000 (first entry)

XX Schizophrenic derived antibody binding epitope #5.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
platelet-associated antibody; diagnosis.

OS Synthetic.

PN WO951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL00190.

PR 02-APR-1998; 98IL-0123925.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

XX New peptides useful for diagnosis of schizophrenia -

PS Claim 3; Page 21; 37pp; English.

XX This sequence is a peptide of the invention, which binds antibodies found
CC in elevated levels in body fluids of schizophrenic patients. The peptide
CC is useful in an assay for the diagnosis of schizophrenia, by binding the
CC peptide to a platelet-containing fraction of blood, or a fraction
CC containing platelet-associated antibodies (PAA) shed from the platelets,
CC or preferably whole blood. The new peptides are able to differentiate
CC between plasma samples from schizophrenic and non-schizophrenic patients,
CC and can do so without having to first isolate the platelet-associated
CC antibodies (PAA) fraction.

SQ Sequence 18 AA;

Query Match 72.2%; Score 65; DB 20; Length 18;

Best Local Similarity 81.2%; Pred. No. 0.013;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGICTGQIKTGAPC 16

Db 2 lvvgictgqiktgapc 17

RESULT 8

ID AAY43194 standard; peptide: 19 AA.

AC AAY43194;

DT 11-JAN-2000 (first entry)

XX Schizophrenic derived antibody binding epitope #4.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
platelet-associated antibody; diagnosis.

OS Synthetic.

XX WO951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL00190.

PR 02-APR-1998; 98IL-0123925.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

XX New peptides useful for diagnosis of schizophrenia -

PS Claim 3; Page 21; 37pp; English.

XX This sequence is a peptide of the invention, which binds antibodies found
CC in elevated levels in body fluids of schizophrenic patients. The peptide
CC is useful in an assay for the diagnosis of schizophrenia, by binding the
CC peptide to a platelet-containing fraction of blood, or a fraction
CC containing platelet-associated antibodies (PAA) shed from the platelets,
CC or preferably whole blood. The new peptides are able to differentiate
CC between plasma samples from schizophrenic and non-schizophrenic patients,
CC and can do so without having to first isolate the platelet-associated
CC antibodies (PAA) fraction.

SQ Sequence 19 AA;

Query Match 72.2%; Score 65; DB 20; Length 19;

Best Local Similarity 81.2%; Pred. No. 0.014;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGICTGQIKTGAPC 16

Db 3 lvvgictgqiktgapc 18

RESULT 9

ID AAY43193 standard; peptide: 20 AA.

AC AAY43193;

DT 11-JAN-2000 (first entry)

XX Schizophrenic derived antibody binding epitope #3.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
platelet-associated antibody; diagnosis.

OS Synthetic.

PN WO951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL00190.

PR 02-APR-1998; 98IL-0123925.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

XX New peptides useful for diagnosis of schizophrenia -

PS Claim 3; Page 21; 37pp; English.

XX This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.
 CC
 SQ Sequence 20 AA;

Query Match 72.2%; Score 65; DB 20; Length 20;
 Best Local Similarity 81.2%; Pred. No. 0.014;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTCOIKTGPAC 16
 ||||| |||||
 Db 4 lvvgltcgtgkgtgac 19

RESULT 10
 AAY43192
 ID AAY43192 standard; peptide; 28 AA.

XX AAY43192;

XX 11-JAN-2000 (first entry)

XX Schizophrenic derived antibody binding epitope #2.

XX Schizophrenic derived antibody; binding epitope; schizophrenia;
 XX platelet-associated antibody; diagnosis.

XX Synthetic.

XX WO9951725-A2.

XX 14-OCT-1999.

XX 30-MAR-1999; 99WO-IL00190.

XX 02-APR-1998; 98IL-0123925.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Shinitzky M, Deckmann M;

XX WPI: 1999-611037/52.

XX New peptides useful for diagnosis of schizophrenia -

XX Claim 3; Page 21; 37pp; English.

XX This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.
 CC
 SQ Sequence 28 AA;

Query Match 72.2%; Score 65; DB 20; Length 28;
 Best Local Similarity 81.2%; Pred. No. 0.019;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTCOIKTGPAC 16
 ||||| |||||
 Db 12 lvvgltcgtgkgtgac 27

RESULT 11
 AAB42064
 ID AAB42064 standard; Protein; 429 AA.

XX AAB42064;

XX 08-FEB-2001 (first entry)

XX Human ORFX ORF1828 polypeptide sequence SEQ ID NO:3656.

XX Human; open reading frame; ORFX; detection; cytosolic; hepatotropic;
 KW vulnery; antipsoptic; antiparkinsonian; neurotropic; neuroprotective;
 KW anticonvulsant; osteopathic; antihypertensive; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antineoplastic;
 KW antiviral; antibacterial; antifungal; antineumatic; antihypertensive;
 KW antineumatic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antineoplastic disease; coagulation;
 KW thrombosis; contraceptive.

XX Homo sapiens.

XX WO200058473-A2.

XX 05-OCT-2000.

XX 31-MAR-2000; 2000WO-US08621.

XX 31-MAR-1999; 99US-0127607.

XX 02-APR-1999; 99US-0127636.

XX 05-APR-1999; 99US-0127728.

XX 30-MAR-2000; 2000US-0540763.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI: 2000-602362/57.

XX N-PSDB; AAC76273.

XX Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -

XX Claim 11; Page 2810-2811; 5507pp; English.

XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytosolic; hepatotropic; vulnery;
 CC antipsoptic; antiparkinsonian; neurotropic; neuroprotective;
 CC osteopathic; anticonvulsant; antihypertensive; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antineoplastic; antibacterial; antiviral; antineumatic; antihypertensive;
 CC antineumatic; gene therapy; cancer; proliferative disorder; hypertension;
 CC neurodegenerative disorder; osteoarthritis; graft vs host disease;
 CC cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 CC cholesterol ester storage; systemic lupus erythematosus; infection;
 CC severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 CC allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 CC bone damage; cartilage damage; antineoplastic disease; coagulation;
 CC thrombosis; contraceptive.

CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.

SO Sequence 429 AA;

Query Match 72.2%; Score 65; DB 21; Length 429;
Best Local Similarity 81.2%; Pred. No. 0.2;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGAPC 16
| | | | | | | | | | | | | | | | | |
Db 379 LVVGLCTGQIKTGAPC 394

RESULT 12
AAW14001
ID AAW14001 standard; Protein; 433 AA.

XX AAW14001;

DT 23-MAY-1997 (first entry)

XX Enolase protein.

KW PCR; polymerase chain reaction; primer; amplify; tyrosine; human; NSE;
KW enolase; radioisotope; antigen.

XX Homo sapiens.

PN JP08308584-A.

PD 26-NOV-1996.

PF 19-MAY-1995; 95JP-0145542.

PR 19-MAY-1995; 95JP-0145542.

PA (EIKE) EIKEN KAGAKU KK.

DR WPI; 1997-059703/06.

PT Introducing tyrosine residues into a protein for radioisotopic
PT labelling - by substitution, addition and/or insertion to a DNA
PT coding for the protein, antigenicity of the protein is unchanged by
PT labelling

PS Disclosure: Page 10-11; 13pp; Japanese.

XX This sequence represents the wild type human enolase (NSE) protein. The
CC primers represented by AAT60282-T60285 were used to amplify tyrosine
CC introduced versions of this sequence. The introduced tyrosine residues
CC combine a radioisotope in such a way as to have no substantial effect on
CC the antigenicity of the protein. The peptides with the introduced
CC tyrosine residue are prepared by expressing a recombinant DNA sequence,
CC where the tyrosine residue has been introduced via an insertion or
CC substitution into the wild type sequence. The peptides can then be used
CC in radioimmunoassays, as the introduction of the label does not alter
CC the antigenicity of the protein.

SO Sequence 433 AA;

Query Match 72.2%; Score 65; DB 18; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.2;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGAPC 16
| | | | | | | | | | | | | | | | | |
Db 383 LVVGLCTGQIKTGAPC 398

RESULT 13
AAW54357
ID AAW54357 standard; protein; 433 AA.

XX AAW54357;

DT 14-AUG-1998 (first entry)

XX Alpha Enolase.

KW Endometrium; hyperplasia; adenocarcinoma; proliferative phase;
KW 2D gel electrophoresis; detection.

XX Homo sapiens.

PN WO9810291-A1.

PD 12-MAR-1998.

PF 05-SEP-1997; 97WO-GB02394.

PR 08-APR-1997; 97GB-0007132.

PR 06-SEP-1996; 96GB-0018600.

PA (CLIN-) CENT CLINICAL & BASIC RES.

PI Byrjalsen I, Fey SJ, Larsen P;

DR WPI; 1998-207057/18.

PT Biochemical markers of human endometrium - useful for, e.g.
PT diagnosis of hyperplasia and adenocarcinoma

PS Disclosure: Page 21; 77pp; English.

CC Proteins AAW54349-W54364 are examples of proteins produced in the
CC endometrium during the hyperplasia, adenocarcinoma or proliferative
CC phase of the endometrium. The presence and quantities of these proteins
CC can be detected using 2D gel electrophoresis comparison of cell lysates.
CC The proteins can be used as biochemical markers to detect the phase of
CC the endometrium and can be measured in body fluids, obviating the need
CC for endometrial biopsies.

SO Sequence 433 AA;

Query Match 72.2%; Score 65; DB 19; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.2;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGAPC 16
| | | | | | | | | | | | | | | | | |
Db 383 LVVGLCTGQIKTGAPC 398

RESULT 14
AAV43200
ID AAV43200 standard; peptide; 16 AA.

XX AAV43200;

DT 11-JAN-2000 (first entry)

XX Schizophrenic derived antibody binding epitope #10.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
KW platelet-associated antibody; diagnosis.

XX Synthetic.

PN WO9951725-A2.

PD 14-OCT-1999.
XX 30-MAR-1999; 99WO-IL00190.
XX 02-APR-1998; 98IL-0123925.
XX (YEDA) YEDA RES & DEV CO LTD.
XX Shinitzky M, Deckmann M;
XX WPI; 1999-611037/52.
DR New peptides useful for diagnosis of schizophrenia -
XX
XX
PS Claim 4; Page 21; 37pp; English.
XX
XX This sequence is a peptide of the invention, which binds antibodies found
CC in elevated levels in body fluids of schizophrenic patients. The peptide
CC is useful in an assay for the diagnosis of schizophrenia, by binding the
CC peptide to a platelet-containing fraction of blood, or a fraction
CC containing platelet-associated antibodies (PAA) shed from the platelets,
CC or preferably whole blood. The new peptides are able to differentiate
CC between plasma samples from schizophrenic and non-schizophrenic patients,
CC and can do so without having to first isolate the platelet-associated
CC antibodies (PAA) fraction.
XX
SQ Sequence 16 AA;

Query Match 67.8%; Score 61; DB 20; Length 16;
Best Local Similarity 80.0%; Pred. No. 0.042;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 VVGLCTCQIKTGAPC 16
| | | | | | | | | | | | | | | |
Db 1 vvglctgqiktgapc 15

RESULT 15

AAV43203
ID AAV43203 standard; peptide; 15 AA.

XX
AC AAV43203;

XX
DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #13.

XX Schizophrenic derived antibody; binding epitope; schizophrenia;
KW platelet-associated antibody; diagnosis.

XX
OS Synthetic.

XX
PN W09951725-A2.

XX
PD 14-OCT-1999.

XX
PF 30-MAR-1999; 99WO-IL00190.

XX
PR 02-APR-1998; 98IL-0123925.

XX
PA (YEDA) YEDA RES & DEV CO LTD.

XX
PI Shinitzky M, Deckmann M;

XX
DR WPI; 1999-611037/52.

XX
PT New peptides useful for diagnosis of schizophrenia -

XX
PS Claim 4; Page 21; 37pp; English.

CC This sequence is a peptide of the invention, which binds antibodies found
CC in elevated levels in body fluids of schizophrenic patients. The peptide

CC is useful in an assay for the diagnosis of schizophrenia, by binding the
CC peptide to a platelet-containing fraction of blood, or a fraction
CC containing platelet-associated antibodies (PAA) shed from the platelets,
CC or preferably whole blood. The new peptides are able to differentiate
CC between plasma samples from schizophrenic and non-schizophrenic patients,
CC and can do so without having to first isolate the platelet-associated
CC antibodies (PAA) fraction.
XX
SQ Sequence 15 AA;

Query Match 64.4%; Score 58; DB 20; Length 15;
Best Local Similarity 92.3%; Pred. No. 0.1;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTG 13
| | | | | | | | | | | | | | | |
Db 1 lvvglctgqiktg 13

Search completed: May 8, 2002, 11:45:08
Job time: 209 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 8, 2002, 11:46:35 ; Search time 22.88 Seconds
(without alignments)
102.288 Million cell updates/sec

Title: US-09-647-457-2
Perfect score: 16
Sequence: 1 LVVGLCTQIKTGPAC 16

Scoring table: OLIGO
Gapop 60.0 , Gapept 60.0

Searched: 473505 seqs, 146272329 residues

Word size : 0

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organellar:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	43.8	154	4 Q9NPL4	Q9NPL4 homo sapien
2	7	43.8	159	4 Q9NG70	Q9NG70 peripatus s
3	7	43.8	251	5 Q9NG71	Q9NG71 limulus pol
4	7	43.8	272	4 Q9BT62	Q9BT62 homo sapien
5	7	43.8	353	11 Q9SKT7	Q9SKT7 mus musculu
6	7	43.8	373	13 Q9W6D3	Q9W6D3 pelusios su
7	7	43.8	373	13 Q9W6D2	Q9W6D2 trachemys s
8	7	43.8	373	13 Q9W6D1	Q9W6D1 eumeces ine
9	7	43.8	373	13 Q9W6D0	Q9W6D0 sphenodon p
10	7	43.8	373	13 Q9W6C9	Q9W6C9 calman croc
11	7	43.8	383	5 Q9NG67	Q9NG67 tomocerus s
12	7	43.8	394	13 Q9PTX6	Q9PTX6 lampetra re
13	7	43.8	395	13 Q9PTX5	Q9PTX5 lampetra re
14	7	43.8	395	13 Q9U5F7	Q9U5F7 eptatretus
15	7	43.8	434	5 Q96556	Q96556 penaeus mon
16	7	43.8	434	13 Q9W7L2	Q9W7L2 sceloporos
17	7	43.8	434	13 Q9W7L1	Q9W7L1 trachemys s
18	7	43.8	434	13 Q9W7L0	Q9W7L0 python regi
19	7	43.8	434	13 Q9PVK2	Q9PVK2 alligator m

RESULT	ID	Q9NPL4	PRELIMINARY:	PRT:	154 AA.
20	6	37.5	81	5	Q9Y0A9
21	6	37.5	82	5	Q9U6U0
22	6	37.5	230	2	Q9EXH5
23	6	37.5	517	10	Q9SAD9
24	6	37.5	602	12	Q9QPU9
25	6	37.5	727	10	Q9SVH3
26	6	37.5	1242	12	Q9PZW7
27	6	37.5	1242	12	Q9PZW6
28	6	37.5	2137	4	Q15021
29	5	31.2	33	6	Q9RSD2
30	5	31.2	34	3	Q9URB2
31	5	31.2	36	2	Q9A5R6
32	5	31.2	43	13	Q9PW52
33	5	31.2	55	5	P81902
34	5	31.2	56	10	Q9MB34
35	5	31.2	58	4	Q9P0Z4
36	5	31.2	63	4	Q60770
37	5	31.2	71	12	Q84043
38	5	31.2	72	9	Q80086
39	5	31.2	73	12	Q98181
40	5	31.2	74	2	Q990R4
41	5	31.2	79	4	Q9H493
42	5	31.2	80	8	Q47957
43	5	31.2	81	13	Q9PVS5
44	5	31.2	85	1	Q26173
45	5	31.2	88	2	Q9KMK7

ALIGNMENTS

RESULT 1
Q9NPL4
ID Q9NPL4
AC Q9NPL4
DT 01-OCT-2000 (TREMREL, 15, Created)
DT 01-OCT-2000 (TREMREL, 15, Last sequence update)
DT 01-JUN-2001 (TREMREL, 17, Last annotation update)
DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Andreu N., Estivill X., Escarceller M., Sunoy L.;
RN Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Auffray C., Ansoerge W., Ballabio A., Estivill X., Gibson K.,
RA Lehrach H., Poustka A., Lundeberg J.;
RT "The European IMAGE consortium for integrated molecular analysis of human gene transcripts.";
RT Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
DR EMBL: AL359213; CAB94588.1;
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR PRINTS: PR00148; ENOLASE.
DR PRODOM: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW Glycolysis; Lyase; Magnesium.
FT NON_TER 1
SQ SEQUENCE 154 AA; 16937 MW; 347B95809B1C864D CRC64;

Query Match 43.8%; Score 7; DB 4; Length 154;
 Best Local Similarity 100.0%; Pred. No. 3.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
 |||||
 DB 104 LVVGLCT 110

RESULT 2

O9NG70

PRELIMINARY; PRT; 159 AA.

AC O9NG70; PRELIMINARY; PRT; 159 AA.
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
 OS Peripatus sp. 'Per3'.
 OC Eukaryota; Metazoa; Onychophora; Peripatidae; Peripatus.
 OX NCBI_TaxID=126380;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PER3248.407;
 RA Regier J.C., Shultz J.W.;
 RT "Enolase as a phylogenetic marker."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1 CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1 COPROCTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1 PATHWAY: GLYCOLYSIS.
 CC -1 SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1 SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1 SIMILARITY: TO THE ENOLASE FAMILY.
 DR EMBL: AF258667; AAF72638.1; -.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR ProDom: PD000902; ENOLASE; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 DR GlycoLysis: Lyase; Magnesium.
 FT NON_TER 1 159
 FT NON_TER 1 159
 SQ SEQUENCE 159 AA; 17582 MW; 840E266ACD36D3CD CRC64;

Query Match 43.8%; Score 7; DB 5; Length 159;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
 |||||
 DB 138 LVVGLCT 144

RESULT 3

O9NG71

PRELIMINARY; PRT; 251 AA.

AC O9NG71; PRELIMINARY; PRT; 251 AA.
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
 OS Limulus polyphemus (Atlantic horseshoe crab).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
 OC Limulidae; Limulus.
 OX NCBI_TaxID=6850;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LPO156_406;

RA Regier J.C., Shultz J.W.;
 RT "Enolase as a phylogenetic marker."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1 CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1 COPROCTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1 PATHWAY: GLYCOLYSIS.
 CC -1 SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1 SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1 SIMILARITY: TO THE ENOLASE FAMILY.
 DR EMBL: AF258666; AAF72637.2; -.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR ProDom: PD000902; ENOLASE; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 DR GlycoLysis: Lyase; Magnesium.
 FT NON_TER 1 251
 FT NON_TER 1 251
 SQ SEQUENCE 251 AA; 27452 MW; DEE7B1BA7A87693F CRC64;

Query Match 43.8%; Score 7; DB 5; Length 251;
 Best Local Similarity 100.0%; Pred. No. 5.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
 |||||
 DB 230 LVVGLCT 236

RESULT 4

O9BT62

PRELIMINARY; PRT; 272 AA.

AC O9BT62; PRELIMINARY; PRT; 272 AA.
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE UNKNOWN (PROTEIN FOR IMAGE:3629132) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=CHORIOCARCINOMA;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC004325; AA04325.1; -.
 FT NON_TER 1 272
 FT NON_TER 1 272
 SQ SEQUENCE 272 AA; 29883 MW; 08F1755ADEA88D0C CRC64;

Query Match 43.8%; Score 7; DB 4; Length 272;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
 |||||
 DB 222 LVVGLCT 228

RESULT 5

O99KT7

PRELIMINARY; PRT; 353 AA.

AC O99KT7; PRELIMINARY; PRT; 353 AA.
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE SIMILAR TO ENOLASE 1, ALPHA NON-NEURON (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC004017; AA04017.1; -
 FT NON_TER 1
 SQ SEQUENCE 353 AA; 38299 MW; 2DBD375CE1C26A43 CRC64;

Query Match 43.8%; Score 7; DB 11; Length 353;
 Best Local Similarity 100.0%; Pred. No. 7.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVGLCT 7
 Db 303 LVGLCT 309

RESULT 6
 ID Q9W6D3 PRELIMINARY; PRT; 373 AA.
 AC Q9W6D3;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
 OS Pelusios subdiger.
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Testudines; Pleurodira; Pelomedusidae; Pelusios.
 OX NCB1_TaxID=88690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-99141276; PubMed-9974396;
 RX Hedges S.B., Poling L.L.;
 RT "A molecular phylogeny of reptiles."
 RL Science 283:998-1001(1999).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
 DR EMBL; AF115859; AAD20346.1; -
 DR HSSP; P56252; 1PDZ.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR PRODOM: PD000902; Enolase; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 KW Glycolysis; Lyase; Magnesium.
 FT NON_TER 1
 FT ACT_SITE 373 373
 FT METAL 322 322
 FT METAL 334 334
 SQ SEQUENCE 373 AA; 40259 MW; 39B5C8BB467BD04 CRC64;

Query Match 43.8%; Score 7; DB 13; Length 373;
 Best Local Similarity 100.0%; Pred. No. 7.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVGLCT 7
 Db 365 LVGLCT 371

RESULT 7
 Q9W6D2

ID Q9W6D2 PRELIMINARY; PRT; 373 AA.
 AC Q9W6D2;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
 OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Testudines; Cryptodira; Testudinoidea; Emydidae; Trachemys.
 OX NCB1_TaxID=34903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-99141276; PubMed-9974396;
 RX Hedges S.B., Poling L.L.;
 RT "A molecular phylogeny of reptiles."
 RL Science 283:998-1001(1999).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
 DR EMBL; AF115858; AAD20345.1; -
 DR HSSP; P56252; 1PDZ.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR PRODOM: PD000902; Enolase; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 KW Glycolysis; Lyase; Magnesium.
 FT NON_TER 1
 FT ACT_SITE 373 373
 FT METAL 322 322
 FT METAL 334 334
 SQ SEQUENCE 373 AA; 40272 MW; 055BFAF4D64BF99 CRC64;

Query Match 43.8%; Score 7; DB 13; Length 373;
 Best Local Similarity 100.0%; Pred. No. 7.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVGLCT 7
 Db 365 LVGLCT 371

RESULT 8
 ID Q9W6D1 PRELIMINARY; PRT; 373 AA.
 AC Q9W6D1;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
 OS Eumeces inexpectatus (southeastern five-lined skink).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidae;
 OC Scincidae; Eumeces.
 OX NCB1_TaxID=38930;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-99141276; PubMed-9974396;
 RX Hedges S.B., Poling L.L.;
 RT "A molecular phylogeny of reptiles."
 RL Science 283:998-1001(1999).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).

CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
DR EMBL: AF115857; AAD20344.1; -.
DR HSSP: P56252; 1PDZ.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR PRINTS: PR00148; ENOLASE.
DR PRODOM: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KM Glycolysis; Lyase; Magnesium.
FT NON_TER 1
FT ACT_SITE 373 373
FT METAL 334 334
SQ SEQUENCE 373 AA; 40398 MW; 5D46A0D51F63982A CRC64;

Query Match 43.8%; Score 7; DB 13; Length 373;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7
Db 365 LVVGLCT 371

RESULT 9
Q9W6D0 PRELIMINARY; PRT; 373 AA.
AC Q9W6D0;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ALPHA ENOLASE (FRAGMENT).
OS Sphenodon punctatus (Hatteria) (Tuatara).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Lepidosauria; Rhynchocephalia; Sphenodontidae; Sphenodon.
NCBI_TaxID=8508;
RN [1]
RX SEQUENCE FROM N.A.
RP MEDLINE-99141276; PubMed-9974396;
RA Hedges S.B., Poling L.L.;
RT "A molecular phylogeny of reptiles.";
RL Science 283:998-1001(1999).
DR EMBL: AF115856; AAD20343.1; -.
DR HSSP: P56252; 1PDZ.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR PRINTS: PR00148; ENOLASE.
DR PRODOM: PD000902; Enolase; 1.
FT NON_TER 1
FT ACT_SITE 373 373
SQ SEQUENCE 373 AA; 40440 MW; 1B8D2143C83F865D CRC64;

Query Match 43.8%; Score 7; DB 13; Length 373;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7
Db 365 LVVGLCT 371

RESULT 10
Q9W6C9 PRELIMINARY; PRT; 373 AA.
AC Q9W6C9;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-
DE GLYCERATE HYDRO-LYASE) (FRAGMENT).
OS Caiman crocodilus (Spectacled caiman) (Caiman sclerops).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Caiman.
NCBI_TaxID=8499;
RN [1]
RX SEQUENCE FROM N.A.
RP MEDLINE-99141276; PubMed-9974396;
RA Hedges S.B., Poling L.L.;
RT "A molecular phylogeny of reptiles.";
RL Science 283:998-1001(1999).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE +
H(2O).
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
DR EMBL: AF115855; AAD20342.1; -.
DR HSSP: P56252; 1PDZ.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR PRINTS: PR00148; ENOLASE.
DR PRODOM: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KM Glycolysis; Lyase; Magnesium.
FT NON_TER 1
FT ACT_SITE 373 373
FT METAL 334 334
SQ SEQUENCE 373 AA; 40396 MW; 9F9020B86F66657A CRC64;

Query Match 43.8%; Score 7; DB 13; Length 373;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7
Db 365 LVVGLCT 371

RESULT 11
Q9NG67 PRELIMINARY; PRT; 383 AA.
AC Q9NG67;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-
DE GLYCERATE HYDRO-LYASE) (FRAGMENT).
OS Tomocerus sp. 'Tom'.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Collembola;
OC Arthropoda; Insecta; Entomobryoidae; Tomoceridae; Tomocerus.
NCBI_TaxID=111305;
RN [1]
RX SEQUENCE FROM N.A.
RP STRAIN=TM23_406;
RA Regier J.C., Shultz J.W.;
RT "Enolase as a phylogenetic marker";
RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE +
H(2O).
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
DR EMBL: AF258670; AAF72641.1; -.
DR InterPro: IPR000941; Enolase.

DR Pfam: PF00113; enolase; 1.
DR PRINTS: PR00148; ENOLASE.
DR PRODOM: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW GLYCOLYSIS; Lyase; Magnesium.
FT NON_TER 1
FT NON_TER 383
SQ SEQUENCE 383 AA; 41326 MW; 4523F005F6A5E579 CRC64;

Query Match 43.8%; Score 7; DB 5; Length 383;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
Db 363 LVVGLCT 369

RESULT 12
O9PTX6 PRELIMINARY; PRT; 394 AA.
AC O9PTX6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
GN ENOLASE-1.
OS Lampetra reissneri.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Lampetra.
OX NCBI_TaxID=7753;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20063780; PubMed=10594174;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded genes";
RL J. Mol. Evol. 49:729-735(1999).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
DR EMBL; AB025329; BAA88482.1; -.
DR HSSP; P56252; 1PD2.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR PRINTS: PR00148; ENOLASE.
DR PRODOM: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW GLYCOLYSIS; Lyase; Magnesium.
FT NON_TER 1
FT NON_TER 383
SQ SEQUENCE 394 AA; 42583 MW; BC585FEC712A3D2 CRC64;

DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
GN ENOLASE-2.
OS Lampetra reissneri.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Lampetra.
OX NCBI_TaxID=7753;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20063780; PubMed=10594174;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded genes";
RL J. Mol. Evol. 49:729-735(1999).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
DR EMBL; AB025330; BAA88483.1; -.
DR HSSP; P56252; 1PD2.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR PRINTS: PR00148; ENOLASE.
DR PRODOM: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW GLYCOLYSIS; Lyase; Magnesium.
FT NON_TER 1
FT NON_TER 395
SQ SEQUENCE 395 AA; 43266 MW; 8591D68662DA8544 CRC64;

Query Match 43.8%; Score 7; DB 13; Length 395;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
Db 345 LVVGLCT 351

RESULT 14
O905F7 PRELIMINARY; PRT; 395 AA.
AC O905F7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
OS Eptatretus burgeri (Inshore hagfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Hyperoartia; Myxiniiformes;
OC Myxiniidae; Eptatretinae; Eptatretus.
OX NCBI_TaxID=7764;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20063780; PubMed=10594174;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded genes";
RL J. Mol. Evol. 49:729-735(1999).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).

Search completed: May 8, 2002, 11:48:28
Job time: 113 sec

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
DR EMBL: AB025326; BAA8479.1; -.
DR HSSP: P56252; 1PDZ.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase.1.
DR PRINTS: PR00148; ENOLASE.
DR ProDom: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW Glycolysis; Lyase; Magnesium.
FT NON_TER 1
SQ SEQUENCE 395 AA; 43131 MW; D351C670DDC75CD CRC64;

Query Match 43.8%; Score 7; DB 13; Length 395;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
|||||
DB 345 LVVGLCT 351

RESULT 15
ID 096656 PRELIMINARY; PRT; 434 AA.
AC 096656;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE "ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-ABDOMINAL MUSCLES;
RA Boonchouy C., Boonaywan B., Panyim S., Sonthayanon B.;
RT "Complete cDNA sequence of phosphopyruvate hydratase (enolase) from a marine shrimp, Penaeus monodon.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC EMBL: AF100985; AAC78141.1; -.
DR HSSP: P56252; 1PDZ.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase.1.
DR PRINTS: PR00148; ENOLASE.
DR ProDom: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW Glycolysis; Lyase; Magnesium; Pyruvate.
FT ACT_SITE 343 343 BY SIMILARITY.
FT METAL 353 353 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 434 AA; 47265 MW; EB575CFB541ABD3 CRC64;

Query Match 43.8%; Score 7; DB 5; Length 434;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
|||||
DB 386 LVVGLCT 392

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 8, 2002, 11:44:24 ; Search time 23.05 Seconds
(without alignments)
101.534 Million cell updates/sec

Title: US-09-647-457-2
Perfect score: 90
Sequence: 1 LVVGLCTCQIKTGPAC 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	72.2	154	4	Q9NP14
2	65	72.2	159	5	Q9NG70
3	65	72.2	272	4	Q9BT62
4	65	72.2	353	11	Q99KT7
5	65	72.2	383	5	Q9NG67
6	65	72.2	394	13	Q9PTX6
7	65	72.2	395	13	Q9PTX5
8	65	72.2	395	13	Q9USF7
9	65	72.2	434	5	Q96556
10	65	72.2	434	13	Q9W7L2
11	65	72.2	434	13	Q9W7L1
12	65	72.2	434	13	Q9W7L0
13	65	72.2	434	13	Q9PVK2
14	58	64.4	251	5	Q9NG71
15	55	61.1	159	5	Q9NG73
16	55	61.1	384	5	Q9NG68
17	55	61.1	413	5	Q44100
18	55	61.1	413	5	Q44101
19	55	61.1	433	5	Q9VQ38

20	53	58.9	433	3	Q93873	Q93873 pneumocysti
21	53	58.9	444	5	Q9BPL7	Q9BPL7 toxoplasma
22	51	56.7	326	10	Q42887	Q42887 lycopersico
23	51	56.7	444	10	Q9MA34	Q9MA34 lupinus lut
24	49	54.4	444	10	Q9LEB0	Q9LEB0 spirinacta oi
25	48	53.3	162	5	Q9NG64	Q9NG64 speleonecte
26	48	53.3	385	5	Q9NG69	Q9NG69 polyxenys f
27	47.5	52.8	1664	5	Q9VVO2	Q9VVO2 caenorhabdi
28	47.5	52.8	2945	5	Q18857	Q18857 caenorhabdi
29	47	52.2	429	5	Q9N997	Q9N997 leishmania
30	47	52.2	439	5	Q9U615	Q9U615 mastigamoeb
31	47	52.2	446	5	Q9UAL5	Q9UAL5 plasmodium
32	46	51.1	137	10	Q9T0P1	Q9T0P1 triticum ae
33	46	51.1	137	10	Q9S9D7	Q9S9D7 hordeum vul
34	46	51.1	477	10	Q9SC94	Q9SC94 hordeum vul
35	45.5	50.6	317	13	Q9MBE0	Q9MBE0 brachydanto
36	45.5	50.6	318	13	Q9B0K2	Q9B0K2 brachydanto
37	45	50.0	90	10	Q9S6Y2	Q9S6Y2 triticum ae
38	45	50.0	234	10	Q9ATV6	Q9ATV6 arabidopsis
39	45	50.0	396	12	Q9YK89	Q9YK89 rubella vir
40	44	48.9	43	4	Q99225	Q99225 homo sapien
41	44	48.9	427	4	Q9H152	Q9H152 homo sapien
42	44	48.9	678	4	Q9Y6P2	Q9Y6P2 homo sapien
43	43	47.8	85	2	Q07207	Q07207 mycobacteri
44	43	47.8	429	5	Q9NDH8	Q9NDH8 trypanosoma
45	43	47.8	444	5	Q9UAE6	Q9UAE6 toxoplasma

ALIGNMENTS

RESULT 1

ID	Q9NP14	PRELIMINARY:	PRT:	154 AA.
AC	Q9NP14			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).			
DE	Glycerate hydro-lyase (human).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Andreu N., Estivill X., Escarceller M., Sunoy L.;			
RL	Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Auffray C., Ansoorge W., Ballabio A., Estivill X., Gibson K.,			
RA	Lehrach H., Poustka A., Lundeberg J.;			
RT	"The European IMAGE consortium for integrated Molecular analysis of human gene transcripts.";			
RL	Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.			
CC	-1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H2O.			
CC	-1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).			
CC	-1- PATHWAY: GLYCOLYSIS.			
CC	-1- SUBUNIT: HOMODIMER (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).			
CC	-1- SIMILARITY: TO THE ENOLASE FAMILY.			
DR	EMBL: AL359213; CAB94588.1; -			
DR	InterPro: IPR000941; Enolase.			
DR	Pfam: PF00113; enolase; 1.			
DR	PRINTS: PR00148; ENOLASE.			
DR	ProDom: PD000902; ENOLASE; 1.			
DR	PROSITE: PS00164; ENOLASE; 1.			
KW	Glycolysis; Lyase; Magnesium.			
FT	NON_TER			
SQ	SEQUENCE 154 AA; 16937 MW; 347B95809B1C664D CRC64;			

Query Match 72.2%; Score 65; DB 4; Length 154;
Best Local Similarity 81.2%; Pred. No. 0.00061;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
|||||
DB 104 LVVGLCTGQIKTGAPC 119

RESULT 2

09NG70 PRELIMINARY; PRT; 159 AA.

AC 09NG70; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
OS Peripatus sp. 'Per3'.
OC Eukaryota; Metazoa; Onychophora; Peripatidae; Peripatus.
OX NCBI_TaxID=126380;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PER3248_407;
RA Regier J.C., Shultz J.W.;
RT "Enolase as a phylogenetic marker."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1 CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSHOENOLPYRUVATE + H(2)O.
CC -1 COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
CC -1 PATHWAY: GLYCOLYSIS.
CC -1 SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1 SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1 SIMILARITY: TO THE ENOLASE FAMILY.
DR EMBL; AF258667; AAF72638.1; -.
DR InterPro; IPR000941; Enolase.
DR Pfam; PF00113; enolase; 1.
DR PRINTS; PR00148; ENOLASE.
DR PRODOM; PD000902; Enolase; 1.
DR PROSITE; PS00164; ENOLASE; 1.
KW GLYCOLYSIS; Lyase; Magnesium.
FT NON_TER 1
FT NON_TER 159
SQ SEQUENCE 159 AA; 17582 MW; 840E266ACD36D3CD CRC64;

Query Match 72.2%; Score 65; DB 5; Length 159;
Best Local Similarity 81.2%; Pred. No. 0.00063;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
|||||
DB 138 LVVGLCTGQIKTGAPC 153

RESULT 3

09BT62 PRELIMINARY; PRT; 272 AA.

AC 09BT62; 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
UNKNOWN (PROTEIN FOR IMAGE:3629132) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CHORIOCARCINOMA;
RA Strausberg R.;

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004325; AAH04325.1; -.
FT NON_TER 1
SQ SEQUENCE 272 AA; 29883 MW; 08F1755ADEA8BD0C CRC64;

Query Match 72.2%; Score 65; DB 4; Length 272;
Best Local Similarity 81.2%; Pred. No. 0.00098;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
|||||
DB 222 LVVGLCTGQIKTGAPC 237

RESULT 4

099KT7 PRELIMINARY; PRT; 353 AA.

AC 099KT7; 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
SIMILAR TO ENOLASE 1, ALPHA NON-NEURON (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004017; AAH04017.1; -.
FT NON_TER 1
FT NON_TER 353
SQ SEQUENCE 353 AA; 38299 MW; 2DBD375CE1C26A43 CRC64;

Query Match 72.2%; Score 65; DB 11; Length 353;
Best Local Similarity 81.2%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
|||||
DB 303 LVVGLCTGQIKTGAPC 318

RESULT 5

09NG67 PRELIMINARY; PRT; 383 AA.

AC 09NG67; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
OS Tomocerus sp. 'Tom'.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Collembola; Arthropoleona; Entomobryoidae; Tomoceridae; Tomocerus.
OX NCBI_TaxID=111305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TOM23_406;
RA Regier J.C., Shultz J.W.;
RT "Enolase as a phylogenetic marker."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1 CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSHOENOLPYRUVATE + H(2)O.
CC -1 COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
CC -1 PATHWAY: GLYCOLYSIS.
CC -1 SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1 SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1 SIMILARITY: TO THE ENOLASE FAMILY.
DR EMBL; AF258670; AAF72641.1; -.

DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase: 1.
 DR PRINTS: PR00148; ENOLASE.
 DR ProDom: PD000902; Enolase: 1.
 DR PROSITE: PS00164; ENOLASE: 1.
 KW Glycolysis; Lyase; Magnesium.
 FT NON_TER 1
 FT NON_TER 383
 SQ SEQUENCE 383 AA; 41326 MW; 4523P005F6A5E579 CRC64;

Query Match 72.2%; Score 65; DB 5; Length 383;
 Best Local Similarity 81.2%; Pred. No. 0.0013;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGAPC 16
 Db 363 LVVGLCTCQIKTGAPC 378

RESULT 6
 Q9PTX6 PRELIMINARY; PRT; 394 AA.

AC Q9PTX6; 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
 GN ENOLASE-1.
 OS Lampetia reissneri.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Lampetra.
 OX NCBI_Taxid=7753;
 RN [1]
 RP MEDLINE=20063780; PubMed=10594174;
 RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
 RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded RT genes."
 RL J. Mol. Evol. 49:729-735(1999).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 DR EMBL: AB025330; BAA8483.1; -.
 DR HSSP: P56252; 1PDZ.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase: 1.
 DR PRINTS: PR00148; ENOLASE.
 DR ProDom: PD000902; Enolase: 1.
 DR PROSITE: PS00164; ENOLASE: 1.
 KW Glycolysis; Lyase; Magnesium.
 FT NON_TER 1
 FT NON_TER 394
 SQ SEQUENCE 394 AA; 42583 MW; BC585FE6C712A3D2 CRC64;

Query Match 72.2%; Score 65; DB 13; Length 394;
 Best Local Similarity 81.2%; Pred. No. 0.0013;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGAPC 16
 Db 345 LVVGLCTCQIKTGAPC 360

RESULT 7
 Q9PTX5 PRELIMINARY; PRT; 395 AA.

AC Q9PTX5; 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
 GN ENOLASE-2.
 OS Lampetia reissneri.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Lampetra.
 OX NCBI_Taxid=7753;
 RN [1]
 RP MEDLINE=20063780; PubMed=10594174;
 RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
 RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded RT genes."
 RL J. Mol. Evol. 49:729-735(1999).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 DR EMBL: AB025330; BAA8483.1; -.
 DR HSSP: P56252; 1PDZ.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase: 1.
 DR PRINTS: PR00148; ENOLASE.
 DR ProDom: PD000902; Enolase: 1.
 DR PROSITE: PS00164; ENOLASE: 1.
 KW Glycolysis; Lyase; Magnesium.
 FT NON_TER 1
 FT NON_TER 395
 SQ SEQUENCE 395 AA; 43266 MW; 8591D6862DA8544 CRC64;

Query Match 72.2%; Score 65; DB 13; Length 395;
 Best Local Similarity 81.2%; Pred. No. 0.0013;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGAPC 16
 Db 345 LVVGLCTCQIKTGAPC 360

RESULT 8
 Q9USE7 PRELIMINARY; PRT; 395 AA.

AC Q9USE7; 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
 OS Epiplatys burgeri (Inshore hagfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;
 OC Myxiniidae; Epiplatrinae; Epiplatrus.
 OX NCBI_Taxid=7764;
 RN [1]
 RP MEDLINE=20063780; PubMed=10594174;
 RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
 RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded RT genes."
 RL J. Mol. Evol. 49:729-735(1999).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
 DR EMBL: AB025326; BAA8479.1; -.
 DR HSSP: P56252; 1PDZ.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR PRODOM: PD000902; ENOLASE; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 DR GLYCOLYSIS: Lyase; Magnesium.
 FT NON_TER 1
 SQ SEQUENCE 395 AA; 43131 MW; D351670DDC75CD CRC64;

Query Match 72.2%; Score 65; DB 13; Length 395;
 Best Local Similarity 81.2%; Pred. No. 0.0013;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
 ||||| |||||
 Db 345 LVVGLCTGQIKTGAPC 360

RESULT 9
 ID 096656 PRELIMINARY; PRT; 434 AA.
 AC 096656;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE).
 OS Penaeus monodon (Penaeid shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea; OC Penaeidae; Penaeus.
 OX NCBI_TaxID=6687;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=ABDOMINAL MUSCLES;
 RA Boonhouy C., Boonyawan B., Panyim S., Sonthayanon B.;
 RT "Complete cDNA sequence of phosphopyruvate hydratase (enolase) from a marine shrimp, Penaeus monodon."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
 DR EMBL: AF100985; AAC78141.1; -.
 DR HSSP: P56252; 1PDZ.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR PRODOM: PD000902; ENOLASE; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 DR GLYCOLYSIS: Lyase; Magnesium.
 DE Glycolysis: Lyase; Magnesium. Pyruvate.
 FT ACT_SITE 343 BY SIMILARITY.
 FT METAL 355 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 434 AA; 47265 MW; EB575C6FB541ABD3 CRC64;

Query Match 72.2%; Score 65; DB 5; Length 434;
 Best Local Similarity 81.2%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
 ||||| |||||
 Db 386 LVVGLCTGQIKTGAPC 401

RESULT 10
 ID 09W7L2 PRELIMINARY; PRT; 434 AA.
 AC 09W7L2;
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE).
 OS Sceloporus undulatus (Eastern fence lizard).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae; OC Sceloporus.
 OX NCBI_TaxID=8520;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MUSCLE;
 RA Mannen H., Li S.S.-L.;
 RT "Molecular evidence for a clade of turtles."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC EMBL: AF072587; AAD41644.1; -.
 DR HSSP: P56252; 1PDZ.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR PRODOM: PD000902; ENOLASE; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 DR GLYCOLYSIS: Lyase; Magnesium.
 FT ACT_SITE 341 BY SIMILARITY.
 FT METAL 353 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 434 AA; 47493 MW; 6E377E0F0A767E11 CRC64;

Query Match 72.2%; Score 65; DB 13; Length 434;
 Best Local Similarity 81.2%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
 ||||| |||||
 Db 384 LVVGLCTGQIKTGAPC 399

RESULT 11
 ID 09W7L1 PRELIMINARY; PRT; 434 AA.
 AC 09W7L1;
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE ALPHA ENOLASE (EC 4.2.1.11).
 OS Trachemys scripta elegans.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Testudines; Cryptodira; Testudinoidae; Emydidae; Trachemys.
 OX NCBI_TaxID=31138;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MUSCLE;
 RA Mannen H., Li S.S.-L.;
 RT "Molecular evidence for a clade of turtles."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR HSSP: P56252; 1PDZ.
 DR InterPro: IPR000941; Enolase.

DR Pfam: PF00113; enolase: 1.
 DR PRINTS: PR00148; ENOLASE.
 DR Prodom: PD000902; Enolase: 1.
 KW Lyase.
 SQ SEQUENCE 434 AA; 47333 MW; 1AF6D392C539DD16 CRC64;

Query Match 72.2%; Score 65; DB 13; Length 434;
 Best Local Similarity 81.2%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LVVGLCTCQIKTGAPC 16
 DB 384 LVVGLCTGQIKTGAPC 399

RESULT 12
 Q9W7L0 PRELIMINARY; PRT; 434 AA.
 AC Q9W7L0; 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE).
 OC Pyruvate.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Boidae; Pythonidae;
 OC Python.
 OX NCBI_Taxid=51751;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MUSCLE;
 RA Mannen H., Li S.S.-L.;
 RT "Molecular evidence for a clade of turtles."
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2O).
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
 DR EMBL: AF072589; AAD41646.1; -.
 DR HSSP: P56252; 1PDZ.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase: 1.
 DR Prodom: PD000902; ENOLASE.
 DR PRINTS: PR00148; ENOLASE.
 DR PROSITE: PS00164; ENOLASE: 1.
 DR KEGG: Glycolysis; Lyase; Magnesium.
 KW ACT_SITE 341
 FT METAL 353
 FT MENTAL 353
 SQ SEQUENCE 434 AA; 47570 MW; F242F93B6D467033 CRC64;

Query Match 72.2%; Score 65; DB 13; Length 434;
 Best Local Similarity 81.2%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LVVGLCTCQIKTGAPC 16
 DB 384 LVVGLCTGQIKTGAPC 399

RESULT 13
 Q9PVK2 PRELIMINARY; PRT; 434 AA.
 AC Q9PVK2; 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)

DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE).
 OS Alligator mississippiensis (American alligator).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylia; Alligatorinae; Alligator.
 OX NCBI_Taxid=8496;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MUSCLE;
 RX MEDLINE-99439677; PubMed=10508547;
 RA Mannen H., Li S.S.-L.;
 RT "Molecular evidence for a clade of turtles."
 RL Mol. Phylogenet. Evol. 13:144-148(1999).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2O).
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 DR EMBL: AF072586; AAD41643.1; -.
 DR HSSP: P56252; 1PDZ.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase: 1.
 DR Prodom: PD000902; ENOLASE.
 DR PRINTS: PR00148; ENOLASE: 1.
 DR PROSITE: PS00164; ENOLASE: 1.
 KW Glycolysis; Lyase; Magnesium.
 SQ SEQUENCE 434 AA; 47322 MW; DFD23524BECF5ECA CRC64;

Query Match 72.2%; Score 65; DB 13; Length 434;
 Best Local Similarity 81.2%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LVVGLCTCQIKTGAPC 16
 DB 384 LVVGLCTGQIKTGAPC 399

RESULT 14
 Q9NG71 PRELIMINARY; PRT; 251 AA.
 AC Q9NG71; 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
 OS Limulus polyphemus (Atlantic horseshoe crab).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
 OX Limulidae; Limulus.
 OX NCBI_Taxid=6850;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LPO156.406;
 RA Regier J.C., Shultz J.W.;
 RT "Enolase as a phylogenetic marker."
 RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2O).
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 DR EMBL: AF258666; AAF72637.2; -.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase: 1.
 DR PRINTS: PR00148; ENOLASE: 1.
 DR Prodom: PD000902; ENOLASE: 1.

DR PROSITE: PS00164; ENOLASE; 1.
 KW Glycolysis; Lyase; Magnesium.
 FT NON_TER 1 1
 FT NON_TER 251 1
 SQ SEQUENCE 251 AA; 27452 MW; DEE7B1BA7A87693F CRC64;

Query Match 64.4%; Score 58; DB 5; Length 251;
 Best Local Similarity 92.3%; Pred. No. 0.016;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTG 13
 |||||
 DB 230 LVVGLCTGQIKTG 242

RESULT 15

Q9NG73 PRELIMINARY; PRT; 159 AA.
 AC Q9NG73;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
 OS Eumesocampa frigidilis.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Diplura; Campodeidae; Eumesocampa.
 OX NCBI_TaxId=109745;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EF248_407;
 RA Regier J.C., Shultz J.W.;
 RT Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
 RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
 CC EMBL; AF258664; AAF72635.1; -.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS; PR00148; ENOLASE.
 DR PRODOM; PD000902; ENOLASE; 1.
 DR PROSITE; PS00164; ENOLASE; 1.
 KW Glycolysis; Lyase; Magnesium.
 FT NON_TER 1 1
 FT NON_TER 159 159
 SQ SEQUENCE 159 AA; 17547 MW; 448E41A6DF664D0 CRC64;

Query Match 61.1%; Score 55; DB 5; Length 159;
 Best Local Similarity 75.0%; Pred. No. 0.037;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTG 16
 |||||
 DB 138 LVVGLSTGQIKTGAPC 153

Search completed: May 8, 2002, 11:46:16
 Job time: 112 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 8, 2002, 11:44:44 ; Search time 10.17 Seconds

(without alignments)
57.683 Million cell updates/sec

Title: US-09-647-457-2

Perfect score: 90

Sequence: 1 LVWGLTCQIKTGPAC 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	82.2	458	1 ENOL_HUMAN	Q05524 homo sapien
2	68	75.6	433	1 ENO_BOVIN	Q9KJ14 bos taurus
3	65	72.2	395	1 ENO_ALMT	P42897 alligator m
4	65	72.2	433	1 ENO_ANAPL	P19140 anas platyr
5	65	72.2	433	1 ENO_CHICK	P51913 gallus gall
6	65	72.2	433	1 ENO_HUMAN	P06733 homo sapien
7	65	72.2	433	1 ENO_MOUSE	P17182 mus musculu
8	65	72.2	433	1 ENO_RAT	P04764 rattus norv
9	65	72.2	433	1 ENO_CHICK	P07322 gallus gall
10	65	72.2	433	1 ENO_HUMAN	P13929 homo sapien
11	65	72.2	433	1 ENO_MOUSE	P21550 mus musculu
12	65	72.2	433	1 ENO_RABIT	P25704 oncotolagus
13	65	72.2	433	1 ENO_RAT	P15429 rattus norv
14	65	72.2	433	1 ENO_HUMAN	P09104 homo sapien
15	65	72.2	433	1 ENO_MOUSE	P17183 mus musculu
16	65	72.2	433	1 ENO_RAT	P07323 rattus norv
17	65	72.2	433	1 ENO_MOUSE	P56252 homarus gam
18	65	72.2	433	1 ENO_XENLA	P08734 xenopus lae
19	65	72.2	434	1 ENO_LOLPE	P02654 loligo peal
20	65	72.2	434	1 ENO_SCHJA	P33676 schistosoma
21	65	72.2	434	1 ENO_SCHJA	Q27877 schistosoma
22	59	65.6	434	1 ENO_SCHJA	Q27591 gallus gall
23	56	62.2	433	1 ENO_CAEL	Q27527 caenorhabd
24	55	61.1	433	1 ENO_DROME	P15007 drosophila
25	53	58.9	431	1 ENO_FASHE	Q27655 fasciola he
26	52	57.8	446	1 ENO_ORYSA	Q43971 oryza sativ
27	51	56.7	436	1 ENO_CUNEL	O74286 cunningham
28	51	56.7	444	1 ENO_ARATH	P23696 arabidopsis
29	51	56.7	444	1 ENO_LYCES	P26300 lycopersico
30	50	55.6	446	1 ENO_MAIZE	P42895 zea mays (m
31	50	55.6	440	1 ENO_ALNGL	Q43321 alnus glut
32	50	55.6	445	1 ENO_HEYBR	Q91e10 heyera bras
33	50	55.6	445	1 ENO2_HEYBR	Q91e19 heyera bras

ALIGNMENTS

34	50	55.6	445	1 ENO_RITCO	P42896 ricinus com
35	49	54.4	436	1 ENO_NEOF	P42894 neocallimas
36	49	54.4	444	1 ENO_MESCR	Q43130 mesembryant
37	49	54.4	446	1 ENO_MAIZE	P26301 zea mays (m
38	48	53.3	372	1 ENO_CHIRE	P31683 chlamydomon
39	47	52.2	436	1 ENO_ENTHI	P51555 entamoeba h
40	47	52.2	446	1 ENO_PLAFA	Q27727 plasmodium
41	46.5	51.7	436	1 ENO_YEAST	P00924 saccharomyc
42	46.5	51.7	436	1 ENO2_YEAST	P00925 saccharomyc
43	46	51.1	126	1 THN1_WHEAT	P01544 triticum ae
44	46	51.1	137	1 THN3_WHEAT	P08772 hordeum vul
45	46	51.1	137	1 THN6_HORVU	P09618 hordeum vul

```

RESULT 1
ID ENOL_HUMAN STANDARD: PRT; 458 AA.
AC Q05524;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALPHA ENOLASE, LUNG SPECIFIC (EC 4.2.1.11) (?-PHOSPHO-D-GLYCERATE
DE HYDRO-LYASE) (NON-NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE).
GN ENO1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Lung fibroblast;
RX MEDLINE=93372640; PubMed=7689884;
RA Verma M., Kurl R.N.;
RT "Human lung enolase: cloning and sequencing of cDNA and its
RT inducibility with dexamethasone.";
RL Biochem. Mol. Biol. Int. 30:293-303(1993).
CC -1 CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
+ H(2O).
CC -1 COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER.
CC -1 PATHWAY: GLYCOLYSIS.
CC -1 SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1 SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC -1 INDUCTION: BY DEXAMETHASONE.
CC -1 SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X66610; CAA47179.1; -.
DR HSSP: P56252; 1PDY.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR PRINTS: PR00148; ENOLASE.
DR PRODOM: PD000902; ENOLASE; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW Lyase; Glycolysis; Magnesium; Multigene family.
FT ACT_SITE 167
FT METAL 254
FT METAL 308
FT METAL 336
FT METAL 336
SQ SEQUENCE 458 AA; 49477 MW; 2550F34A2BF4314 CRC64;

```

Query Match

82.2%; Score 74; DB 1; Length 458;

Best Local Similarity 87.5%; Pred. No. 0.00018;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
| | | | | | | | | | | | | | | | | |
DB 407 LVVGLCTGQIKTGAPC 422

RESULT 2

ENO1_BOVIN STANDARD; PRT; 433 AA.
ID ENO1_BOVIN
AC Q9X5J4;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE).
GN ENO1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Chapman K.L., Newman B., Hillaby M.C., Freemont A.J., Grant M.E.,
RA Boot-Handford R., Wallis G.A.;
RT "Alpha enolase is upregulated in proliferative chondrocytes in the
epiphyseal growth plate and in human osteoarthritic tissue."
RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOPYRUVATE
+ H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
FOUND ONLY IN NERVOUS TISSUE.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.

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CC -----
CC EMBL: AF149256; AAD33073.1; -.
CC DR HSSP: P56252; IPDZ.
CC DR InterPro: IPR000941; Enolase.
CC DR Pfam: PF00113; enolase; 1.
CC DR PRINTS: PRO0146; ENOLASE.
CC KW Lyase; Glycolysis; Magnesium; Multigene family.
CC FT INIT_MET 0
CC FT ACT_SITE 157 157 BY SIMILARITY.
CC FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
CC FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
CC FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
CC SQ SEQUENCE 433 AA; 47145 MW; B004E95C46F2E0C CRC64;

Query Match 75.6%; Score 68; DB 1; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
| | | | | | | | | | | | | | | | | |
DB 383 LVVGLCTGQIKTGAPC 398

RESULT 3

ENO1_ALLMI STANDARD; PRT; 395 AA.
ID ENO1_ALLMI
AC P42697;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94195794; Pubmed=8146164;
RA Hedges S.B.;
RT "Molecular evidence for the origin of birds."
RL Proc. Natl. Acad. Sci. U.S.A. 91:2621-2624(1994).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOPYRUVATE
+ H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.

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CC -----
CC EMBL: L28078; AA53671.1; -.
CC DR HSSP: P56252; IPDZ.
CC DR InterPro: IPR000941; Enolase.
CC DR Pfam: PF00113; enolase; 1.
CC DR ProDom: PD000902; Enolase; 1.
CC DR PROSITE: PS00164; ENOLASE; 1.
CC KW Lyase; Glycolysis; Magnesium.
CC FT NON_TER 1
CC FT ACT_SITE 136 136 BY SIMILARITY.
CC FT METAL 223 223 MAGNESIUM (BY SIMILARITY).
CC FT METAL 271 271 MAGNESIUM (BY SIMILARITY).
CC FT METAL 296 296 MAGNESIUM (BY SIMILARITY).
CC FT NON_TER 395
CC SQ SEQUENCE 395 AA; 42884 MW; B43E91228E9110B5 CRC64;

Query Match 72.2%; Score 65; DB 1; Length 395;
Best Local Similarity 81.2%; Pred. No. 0.004;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
| | | | | | | | | | | | | | | | | |
DB 362 LVVGLCTGQIKTGAPC 377

RESULT 4

ENO1_ANAPL STANDARD; PRT; 433 AA.
ID ENO1_ANAPL
AC P19140;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (TAU-CRYSTALLIN).
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
 OX NCBI_TaxID=8839;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryonic lens;
 RX MEDLINE=89079778; PubMed=2462567;
 RA Wistow G.J., Lietman T., Williams L.A., Stapel S.O., de Jong W.W.,
 RT Horwitz J., Piatigorsky J.;
 RT "tau-crystallin/alpha-enolase: one gene encodes both an enzyme and a
 lens structural protein.";
 RT J. Cell Biol. 107:2729-2736(1988).
 CC -1- FUNCTION: BOTH AN ENZYME AND A LENS STRUCTURAL PROTEIN.
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
 CC + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
 CC THE DIMER.
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: M20749; AAA9218.1; -;
 DR EMBL: X14195; CA32409.1; -;
 DR PIR: A32132; A32132.
 DR HSP: P56252; LPDY.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase.1.
 DR PRINTS: PR00148; ENOLASE.
 DR PRODOM: PD000902; ENOLASE.1.
 DR PROSITE: PS00164; ENOLASE.1.
 KW Lyase; Glycolysis; Magnesium; Eye lens protein.
 FT INIT MET 0
 FT ACT SITE 157 157 BY SIMILARITY.
 FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
 FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
 FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 433 AA; 47108 MW; 1AED7B08A66E84D CRC64;

Query Match 72.2%; Score 65; DB 1; Length 433;
 Best Local Similarity 81.2%; Pred. No. 0.0043;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVGGLCTGQIKTGAPC 16
 DB 383 LVGGLCTGQIKTGAPC 398

RESULT 5
 ENOA_CHICK
 ID ENOA_CHICK STANDARD: PRT; 433 AA.
 AC P51913;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
 DE (PHOSPHOPYRUVATE HYDRATASE).
 OS Gallus gallus (Chicken)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WHITE LEGHORN; TISSUE=Kidney;

RX MEDLINE=95355305; PubMed=7629021;
 RA Tanaka M., Maeda K., Nakashima K.;
 RT "Chicken alpha-enolase but not beta-enolase has a Src-dependent
 RT tyrosine-phosphorylation site: cDNA cloning and nucleotide sequence
 RT analysis.";
 RL J. Biochem. 117:554-559(1995).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
 CC + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
 CC THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: D37900; BA07132.1; -;
 DR HSP: P56252; LPDY.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase.1.
 DR PRINTS: PR00148; ENOLASE.
 DR PRODOM: PD000902; ENOLASE.1.
 DR PROSITE: PS00164; ENOLASE.1.
 KW Lyase; Glycolysis; Magnesium; Multigene family.
 FT INIT MET 0
 FT ACT SITE 157 157 BY SIMILARITY.
 FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
 FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
 FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 433 AA; 47173 MW; 93AD6B0A7AD99910 CRC64;

Query Match 72.2%; Score 65; DB 1; Length 433;
 Best Local Similarity 81.2%; Pred. No. 0.0043;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVGGLCTGQIKTGAPC 16
 DB 383 LVGGLCTGQIKTGAPC 398

RESULT 6
 ENOA_HUMAN
 ID ENOA_HUMAN STANDARD: PRT; 433 AA.
 AC P06735; Q16704; Q9DM55;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-
 DE NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE).
 GN ENO1 OR ENO1L1.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86313654; PubMed=3529090;
 RA Galliongo A., Feo S., Moore R., Croce C.M., Shove L.C.;
 RT "Molecular cloning and nucleotide sequence of a full-length cDNA for
 RT human alpha enolase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:6741-6745(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90323004; PubMed=2373081;
 RA Galliongo A., Oliva D., Cali L., Barba G., Barbieri G., Feo S.;

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RT "Structure of the human gene for alpha-enolase.";
RL Eur. J. Biochem. 190:567-573(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Endometrium; PubMed=8824716;
RX MEDLINE=96422099; PubMed=8824716;
RA Walter M., Leidenberger F.A., Scheppe K.W., Northmann W.;
RT "Autoreactive epitopes within the human alpha-enolase and their
  recognition by sera from patients with endometriosis.";
RL J. Autoimmun. 8:937-945(1995).
RN [4]
RP SEQUENCE OF 165-433 FROM N.A.
RX MEDLINE=98317532; PubMed=9653645;
RA Onyango P., Luboyva B., Gardellin P., Kurzbauer R., Welch A.;
RT "Molecular cloning and expression analysis of five novel genes in
  chromosome 1p36.";
RL Genomics 50:187-198(1998).
RN [5]
RP SEQUENCE OF 269-280 AND 306-320.
RX MEDLINE=95307697; PubMed=7787969;
RA Mohamed R.M., Handan M.Y., Maki A., Al-Kalib A.;
RT "Induced expression of alpha-enolase in differentiated diffuse large
  cell lymphoma.";
RL Enzyme Protein 48:37-44(1995).
RN [6]
RP SEQUENCE OF 1-8.
RC TISSUE=Colon carcinoma; PubMed=9150948;
RX MEDLINE=97295306; PubMed=9150948;
RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
RT "A two-dimensional gel database of human colon carcinoma proteins.";
RL Electrophoresis 18:605-613(1997).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
  + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
  THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
  IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
  MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
  FOUND ONLY IN NERVOUS TISSUE.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC -----
DR EMBL: M14328; AAA52387.1; -
DR EMBL: X16288; CAA34360.1; -
DR EMBL: X16289; CAA34360.1; JOINED.
DR EMBL: X16290; CAA34360.1; JOINED.
DR EMBL: X84907; CAA59331.1; -
DR EMBL: U88968; AAC39935.1; -
DR PIR: A29170; A29170.
DR PIR: S11696; S11696.
DR HSSP: P56252; IPDY.
DR Aarhus/Chent-2DPAGE; 1325; IEF.
DR Aarhus/Chent-2DPAGE; 5406; NEPHGE.
DR MIM: 172430; -
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase.1.
DR PRINTS: PR00148; ENOLASE.
DR PRODOM: PD000902; ENOLASE.1.
DR PROSITE: PS00164; ENOLASE.1.
KW Lyase; Glycolysis; Magnesium; Multigene family.
FT INIT MET 0
FT ACT SITE 157 157 BY SIMILARITY.
FT METAL 244 244 MAGNESIUM (BY SIMILARITY).

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FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
FT CONFLICT 251 251 F -> S (IN REF. 3).
SO SEQUENCE 433 AA; 47037 MW; B2028684C33140B5 CRC64;

Query Match
Best Local Similarity 72.2%; Score 65; DB 1; Length 433;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTQIKTGAPC 16
Db 383 LVVGLCTQIKTGAPC 398

RESULT 7
ID ENOA_MOUSE STANDARD: PRT: 433 AA.
AC P17182; Q9DCY7;
DT 01-AUG-1990 (Rel. 15, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-
  NEURAL ENOLASE) (NNE).
GN ENOI OR ENO-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
CX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=90301487; PubMed=2362815;
RA Kaghad M., Dumont X., Chalon P., Lelias J.M., Lomande N., Lucas M.,
  Lazar M., Caput D.;
RT "Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from
  mouse brain.";
RL Nucleic Acids Res. 18:3638-3638(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
  Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
  Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
  Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
  Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
  Fletschmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
  Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
  Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
  Sakai K., Boffelli D., Furuno M., Aono H., Baldarelli R., Barsh G.,
  Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
  Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
  Lyons P., Marchionni L., Mashima J., Mazzarelli J., Kombearts P.,
  Nodone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
  Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
  Suzuki H., Toyoko-Oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
  Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
  Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
RL -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
  + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
  THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
  IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
  MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
  FOUND ONLY IN NERVOUS TISSUE.

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CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X53379; CAA36605.1; -
DR EMBL: AK002336; BAB22021.1; -
DR PIR: S10246; S10246.
DR HSSP: P56252; IPDY.
DR SWISS-2DPAGE: P17182; MOUSE.
DR MGD: MGI:95393; Enol.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR PRINTS: PR00148; ENOLASE.
DR ProDom: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
DR Lysase; Glycolysis; Magnesium; Multigene family.
FT INIT_MET 0
FT ACT_SITE 157 157 BY SIMILARITY.
FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
FT CONFLICT 358 358 L -> P (IN REF. 1)
SO SEQUENCE 433 AA; 47009 MW; C90082CBA8290EB6 CRC64;

Query Match 72.2%; Score 65; DB 1; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.0043;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
Db 383 LVVGLCTGQIKTGAPC 398

RESULT 8
ENOA_RAT STANDARD; PRT; 433 AA.
AC P04764;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-
DE NEURAL ENOLASE) (NNE).
GN ENOI OR ENO-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85242108; PubMed=2989793;
RA Sakimura K., Kushiya E., Obinata M., Takahashi Y.;
RT "Molecular cloning and the nucleotide sequence of cDNA to mRNA for
RT non-neuronal enolase (alpha alpha enolase) of rat brain and liver.";
RL Nucleic Acids Res. 13:4365-4378(1985).
RN [2]
RP SEQUENCE FROM N.A.
RA Takahashi Y.;
RT Submitted (JAN-1986) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
CC + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN

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CC IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
CC MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
CC FOUND ONLY IN NERVOUS TISSUE.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X02610; CAA26456.1; -
DR PIR: A23126; A23126.
DR HSSP: P56252; IPDY.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR PRINTS: PR00148; ENOLASE.
DR ProDom: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
DR Lysase; Glycolysis; Magnesium; Multigene family.
FT INIT_MET 0
FT ACT_SITE 157 157 BY SIMILARITY.
FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
SO SEQUENCE 433 AA; 46984 MW; F1A25F010C276E7C CRC64;

Query Match 72.2%; Score 65; DB 1; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.0043;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
Db 383 LVVGLCTGQIKTGAPC 398

RESULT 9
ENOB_CHICK STANDARD; PRT; 433 AA.
AC P07322;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
DE (PHOSPHOPYRUVATE HYDRATASE).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=WHITE LEGHORN; TISSUE=Muscle;
RX MEDLINE=95355305; PubMed=7629021;
RA Tanaka M., Maeda K., Nakashima K.;
RT "Chicken alpha-enolase but not beta-enolase has a Src-dependent
RT lysine-phosphorylation site: cDNA cloning and nucleotide sequence
RT analysis.";
RL J. Biochem. 117:554-559(1995).
RN [2]
RP SEQUENCE.
RX MEDLINE=87075592; PubMed=3539098;
RA Russell G.A., Dunbar B., Fothergill-Gilmore L.A.;
RT "The complete amino acid sequence of chicken skeletal muscle
RT enolase.";
RL Biochem. J. 236:115-126(1986).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
CC + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER.

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CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL: D37901; BAA07133.1; -.
CC PIR: A23850; A23850.
CC HSP: P56252; 1PDY.
CC InterPro: IPR000941; Enolase.
CC Pfam: PF00113; enolase; 1.
CC PRINTS: PR00148; ENOLASE.
CC PRODOM: PD000902; ENOLASE.
CC PROSITE: PS00164; ENOLASE; 1.
CC Lysase, Glycolysis; Magnesium; Multigene family; Acetylation.
CC INIT_MET 0 0
CC MOD_RES 1 1
CC ACT_SITE 157 157 ACETYLATION.
CC METAL 244 244 BY SIMILARITY.
CC METAL 292 292 MAGNESIUM (BY SIMILARITY).
CC METAL 317 317 MAGNESIUM (BY SIMILARITY).
CC METAL 317 317 MAGNESIUM (BY SIMILARITY).
CC CONFLICT 16 16 E -> D (IN REF. 2).
CC CONFLICT 48 48 P -> L (IN REF. 2).
CC CONFLICT 93 93 M -> V (IN REF. 2).
CC CONFLICT 118 119 CK -> SH (IN REF. 2).
CC CONFLICT 208 208 G -> D (IN REF. 2).
CC CONFLICT 257 257 H -> D (IN REF. 2).
CC CONFLICT 265 266 HT -> DP (IN REF. 2).
CC CONFLICT 269 269 Y -> L (IN REF. 2).
CC CONFLICT 308 308 F -> S (IN REF. 2).
CC CONFLICT 322 322 T -> A (IN REF. 2).
CC CONFLICT 330 330 G -> A (IN REF. 2).
CC CONFLICT 342 342 K -> G (IN REF. 2).
CC CONFLICT 393 394 KT -> EO (IN REF. 2).
CC SEQUENCE 433 AA; 47065 MW; 9BC2FB5FB910C254 CRC64;

Query Match 72.2%; Score 65; DB 1; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.0043;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTQIKTGAPC 16
Db 383 LVVGLCTGQIKTGAPC 398

RESULT 10
ENOB_HUMAN STANDARD; PRT; 433 AA.
AC P13929;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 20-ANG-2001 (Rel. 40, Last annotation update)
DE BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
DE (SKELETAL MUSCLE ENOLASE) (MSE).
GN ENO3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90067857; PubMed=2587223;
RA Peshavaria M., Hinks L.J., Day I.N.M.;
RT "Structure of human muscle (beta) enolase mRNA and protein deduced
RT from a genomic clone.";

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RL Nucleic Acids Res. 17:8862-8862(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91222137; PubMed=1840492;
RA Peshavaria M., Day I.N.M.;
RT "Molecular structure of the human muscle-specific enolase gene
RT (ENO3).";
RL Biochem. J. 275:427-433(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=9024587; PubMed=236366;
RA Cali U., Feo S., Oliva D., Giallongo A.;
RT "Nucleotide sequence of a cDNA encoding the human muscle-specific
RT enolase (MSE).";
RL Nucleic Acids Res. 18:1893-1893(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=93292497; PubMed=8513787;
RA Giallongo A., Venturella S., Oliva D., Barbieri G., Rubino P.,
RA Feo S.;
RT "Structural features of the human gene for muscle-specific enolase.
RT Differential splicing in the 5'-untranslated sequence generates two
RT forms of mRNA.";
RL Eur. J. Biochem. 214:367-374(1993).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
CC + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
CC IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
CC MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
CC FOUND ONLY IN NERVOUS TISSUE.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
-----
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-----
CC EMBL: X16504; CAA34513.1; -.
CC EMBL: X51957; CAA36216.1; -.
CC EMBL: X55976; CAA39446.1; -.
CC EMBL: X56832; CAA40163.1; -.
CC PIR: S15933; S15933.
CC PIR: S06756; S06756.
CC PIR: S14759; S14759.
CC PIR: S31650; S31650.
CC PIR: S33330; S33330.
CC HSP: P56252; 1PDY.
CC MIM: 131370; -.
CC InterPro: IPR000941; Enolase.
CC Pfam: PF00113; enolase; 1.
CC PRINTS: PR00148; ENOLASE.
CC PRODOM: PD000902; ENOLASE.
CC PROSITE: PS00164; ENOLASE; 1.
CC Lysase, Glycolysis; Magnesium; Multigene family.
CC INIT_MET 0 0
CC ACT_SITE 157 157 BY SIMILARITY.
CC METAL 244 244 MAGNESIUM (BY SIMILARITY).
CC METAL 292 292 MAGNESIUM (BY SIMILARITY).
CC METAL 317 317 MAGNESIUM (BY SIMILARITY).
CC CONFLICT 84 84 V -> A (IN REF. 3).
CC CONFLICT 161 161 K -> N (IN REF. 1 AND 2).
CC SEQUENCE 433 AA; 46855 MW; 5F726D743DBFB2F CRC64;

Query Match 72.2%; Score 65; DB 1; Length 433;

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Best Local Similarity 81.2%; Pred. No. 0.0043;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1 LVVGLCTGQIKTGAPC 16
DB 383 LVVGLCTGQIKTGAPC 398

RESULT 11
ENOB_MOUSE
ID ENOB_MOUSE STANDARD: PRT: 433 AA.
AC P21550;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
DE (SKELETAL MUSCLE ENOLASE).
GN ENO3 OR ENO-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAIB/C; TISSUE=Liver;
RL Lamande N., Brosset S., Keller A., Lucas M., Lazar M.;
RN Submitted (SEP-1991) to the EMBL/Cenbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H;
RL MEDLINE=92290133; PubMed=1339335;
RA Peterson C.A., Cho M., Rastinejad F., Blau H.M.;
RT "Beta-enolase is a marker of human myoblast heterogeneity prior to
differentiation.";
RN Dev. Biol. 151:626-629(1992).
RN [3]
RP SEQUENCE OF 58-433 FROM N.A.
RL MEDLINE=89282789; PubMed=2734297;
RA Lamande N., Mazo A.M., Lucas M., Montarras D., Pinset C., Gros F.,
RA Legault-Demare L., Lazar M.;
RT "Murine muscle-specific enolase: cDNA cloning, sequence, and
developmental expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:4445-4449(1989).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
+ H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
FOUND ONLY IN NERVOUS TISSUE.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC -----
DR EMBL; X61600; CAA43797.1; -;
DR EMBL; X62657; CAA44540.1; -;
DR EMBL; M20745; AAA37554.1; -;
DR EMBL; X57747; CAA40913.1; -;
DR PIR; S17109; NOKSB.
DR PIR; A33921; A33921.
DR PIR; S29675; S29675.
DR HSSP; P56252; 1PDY.
DR SWISS-2DPAGE; P21550; MOUSE.

DR MGD; MGI:95395; Eno3.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR PRINTS: PRO0148; ENOLASE.
DR ProDom: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW Lyase; Glycolysis; Magnesium; Multigene family.
FT INIT_MET 0
FT ACT_SITE 157 157
FT METAL 244 244
FT METAL 292 292
FT METAL 317 317
FT CONFLICT 233 234
SO SEQUENCE 433 AA; 46893 MW; B318B763382D3FA8 CRC64;
BY SIMILARITY.
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
AG -> NA (IN REF. 3).
Query Match
Best Local Similarity 72.2%; Score 65; DB 1; Length 433;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1 LVVGLCTGQIKTGAPC 16
DB 383 LVVGLCTGQIKTGAPC 398

RESULT 12
ENOB_RABIT
ID ENOB_RABIT STANDARD: PRT: 433 AA.
AC P25704; Q9N0M6;
DT 01-MAY-1992 (Rel. 22, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
DE (SKELETAL MUSCLE ENOLASE).
GN ENO3.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=91113295; PubMed=2275753;
RA Chin C.C.O.;
RT "The primary structure of rabbit muscle enolase.";
RL J. Protein Chem. 9:427-432(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Zheng S.-X.;
RT "The cDNA cloning of rabbit muscle-specific enolase gene, site
directed mutagenesis (P417L) of the gene, expression of the wild-type
and mutant genes in Escherichia coli.";
RL Theslis (1995), Concordia University, Montreal / Quebec, Canada.
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
+ H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
FOUND ONLY IN NERVOUS TISSUE.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC -----

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CC -----
CC EMBL: AF260259; AAF71925.1; -.
CC PIR: A37210; A37210.
CC HSP: P56252; 1PDP.
CC InterPro: IPR000941; Enolase.
CC Pfam: PF00113; enolase; 1.
CC PRINTS: PR00148; ENOLASE.
CC ProDom: PD000902; ENOLASE; 1.
CC PROSITE: PS00164; ENOLASE; 1.
CC Lyase: Glycolysis; Magnesium; Multigene family.
CC INT_MET 0
CC ACT_SITE 157 157 BY SIMILARITY.
CC METAL 244 244 MAGNESIUM (BY SIMILARITY).
CC METAL 292 292 MAGNESIUM (BY SIMILARITY).
CC METAL 317 317 MAGNESIUM (BY SIMILARITY).
CC CONFLICT 253 253 N -> D (IN REF. 1).
CC CONFLICT 296 296 N -> D (IN REF. 1).
CC SEQUENCE 433 AA; 46859 MW; 063A4005443C0403 CRC64;

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Query Match 72.2%; Score 65; DB 1; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.0043;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 LVVGLCTGQIKTGAPC 16
Db 383 LVVGLCTGQIKTGAPC 398

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RESULT 13
ENOB_RAT STANDARD; PRT; 433 AA.
AC P15429;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
DE (SKELETAL MUSCLE ENOLASE).
DE ENO3 OR ENO-3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR;
RX MEDLINE=8912113; PubMed=2914621;
RA Ohshima Y., Mitsui H., Takayama Y., Kushiya E., Sakimura K.,
RA Takahashi Y.;
RT "cDNA cloning and nucleotide sequence of rat muscle-specific enolase
(beta beta enolase).";
RN FEBS Lett. 242:425-430(1989).
[2]
RP SEQUENCE OF 1-27 FROM N.A.
RX MEDLINE=91099531; PubMed=2269373;
RA Sakimura K., Kushiya E., Ohshima-Ichimura Y., Mitsui H.,
RA Takahashi Y.;
RT "Structure and expression of rat muscle-specific enolase gene.";
RN FEBS Lett. 277:78-82(1990)
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
+ H(2O).
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOSOL.
CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
FOUND ONLY IN NERVOUS TISSUE.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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CC -----

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CC EMBL: Y00979; CA68788.1; -.
CC PIR: S02072; S02072.
CC HSP: P56252; 1PDP.
CC InterPro: IPR000941; Enolase.
CC Pfam: PF00113; enolase; 1.
CC PRINTS: PR00148; ENOLASE.
CC ProDom: PD000902; ENOLASE; 1.
CC PROSITE: PS00164; ENOLASE; 1.
CC Lyase: Glycolysis; Magnesium; Multigene family.
CC INT_MET 0
CC ACT_SITE 157 157 BY SIMILARITY.
CC METAL 244 244 MAGNESIUM (BY SIMILARITY).
CC METAL 292 292 MAGNESIUM (BY SIMILARITY).
CC METAL 317 317 MAGNESIUM (BY SIMILARITY).
CC SEQUENCE 433 AA; 46829 MW; 4C2CDBD12DBA536D CRC64;

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Query Match 72.2%; Score 65; DB 1; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.0043;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 LVVGLCTGQIKTGAPC 16
Db 383 LVVGLCTGQIKTGAPC 398

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RESULT 14
ENOB_HUMAN STANDARD; PRT; 433 AA.
AC P09104;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GAMMA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
DE (NEURAL ENOLASE) (NSE).
DE ENO2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC TISSUE=Retina;
RX MEDLINE=89091176; PubMed=3208766;
RA McAliese S.M., Dunbar B., Forthright J., Hinks L., Day I.N.M.;
RT "Complete amino acid sequence of the neurone-specific gamma isozyme
of enolase (NSE) from human brain and comparison with the
non-neuronal alpha form (NNE).";
RN Eur. J. Biochem. 178:413-417(1988).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9006764; PubMed=2792767;
RA Oliva D., Barba G., Bardieri G., Giallongo A., Feo S.;
RT "Cloning, expression and sequence homologies of cDNA for human gamma
enolase.";
RN Gene 79:355-360(1989).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88259288; PubMed=3385803;
RA van Obberghen E., Kamholz J., Bishop J.G. III, Zomzely-Neurath C.,
RA Lazzarini R.A.;
RT "Human gamma enolase: isolation of a cDNA clone and expression in
normal and tumor tissues of human origin.";
RN J. Neurosci. Res. 19:450-456(1988).

```

[4]
 RN SEQUENCE FROM N.A.
 RP TISSUE-Hematopoietic;
 RX MEDLINE=91257823; PubMed=2045099;
 RT Oliva D., Call L., Rao S., Giallongo A.;
 RL "Complete structure of the human gene encoding neuron-specific
 RT enolase.";
 RN Genomics 10:157-165(1991).
 [5]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=96303695; PubMed=8723724;
 RA Ansari-Lari M.A., Muzny D.M., Lu J., Lu F., Lilley C.E.,
 RA Spanos S., Malley T., Gibbs R.A.;
 RT "A gene-rich cluster between the CD4 and triosephosphate isomerase
 RT genes at human chromosome 12p13.";
 RL Genome Res. 6:314-326(1996).
 [6]
 RN SEQUENCE OF 424-433 FROM N.A.
 RX MEDLINE=88005129; PubMed=3653393;
 RA Day I.N.M., Allsopp M.T.E.P., Moore D.C.M., Thompson R.J.;
 RT "Sequence conservation in the 3'-untranslated regions of neurone-
 RT specific enolase, lymphokine and protooncogene mRNAs.";
 RL FEBS Lett. 222:139-143(1987).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
 CC + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
 CC THE DIMER.
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
 CC IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
 CC MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
 CC FOUND ONLY IN NERVOUS TISSUE.
 CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X13120; CAA31512.1; -;
 DR EMBL: M22349; AAB59554.1; -;
 DR EMBL: X51956; AAB52388.1; ALT_INIT.
 DR EMBL: X51956; CAA36215.1; -;
 DR EMBL: U47924; AAB51320.1; -;
 DR EMBL: X14327; CAA32505.1; -;
 DR PIR: J00060; NOHUG.
 DR PIR: S02077; S02077.
 DR PIR: S02616; S02616.
 DR HSSP: P56252; 1PDY.
 DR MIM: 131360; -;
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR ProDom: PD000902; Enolase; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 KW Lyase; Glycolysis; Magnesium; Multigene family; Polymorphism.
 FT INIT_MEN 0
 FT ACCT_SITE 157 157
 FT METAL 244 244
 FT METAL 292 292
 FT METAL 317 317
 FT VARIANT 263 263
 FT VARIANT 394 394
 FT VARIANT 394 394
 FT CONFLICT 3 3
 FT CONFLICT 26 27
 FT CONFLICT 126 126
 E -> N (IN REF. 3).
 E -> N (IN REF. 3).

FT CONFLICT 239 239 M -> I (IN REF. 2, 3, 4 AND 5).
 SQ SEQUENCE 433 AA; 47154 MW; 0F01A8A5FP9152A1 CRC64;
 Query Match 72.2%; Score 65; DB 1; Length 433;
 Best Local Similarity 81.2%; Pred. No. 0.0043;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LVGLCTGQIKTGAPC 16
 Db 383 LVGLCTGQIKTGAPC 398
 RESULT 15
 ENOG_MOUSE
 ID ENOG_MOUSE STANDARD; PRT; 433 AA.
 AC P17183;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GAMMA ENOLASE (RC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
 DE (NEURAL ENOLASE) (NSE).
 GN ENO2 OR ENO-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=90301487; PubMed=2362815;
 RA Raghad M., Dumont X., Chalton P., Lelias J.M., Lamande N., Lucas M.,
 RA Lazar M., Caput D.;
 RT "Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from
 RT mouse brain.";
 RL Nucleic Acids Res. 18:3638-3638(1990).
 [2]
 RN SEQUENCE FROM N.A.
 RA Ansari-Lari M.A., Oeltjen J.C., Schwartz S., Zhang Z., Muzny D.M.,
 RA Lu J., Gorrell J.H., Chinnait A.C., Belmont J.W., Miller W.,
 RA Gibbs R.A.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
 CC + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
 CC THE DIMER.
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
 CC IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
 CC MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
 CC FOUND ONLY IN NERVOUS TISSUE.
 CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X52380; CAA36606.1; -;
 DR EMBL: AC002397; AAC36002.1; -;
 DR PIR: S10247; S10247.
 DR HSSP: P56252; 1PDY.
 DR MGD: MGI:95394; Eno2.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR ProDom: PD000902; Enolase; 1.
 DR PROSITE: PS00164; ENOLASE; 1.

KW Lyase; Glycolysis; Magnesium; Multigene family.
FT INIT_MER 0 0
FT ACT_SITE 157 157 BY SIMILARITY.
FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 433 AA: 47165 MW: B7281132E637D43E CRC64;

Query Match 72.2%; Score 65; DB 1; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.0043;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGAPC 16
|||||
DB 383 LVVGLCTGQIKTGAPC 398

Search completed: May 8, 2002, 11:46:32
Job time: 108 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 8, 2002, 11:45:50 ; Search time 12.85 Seconds

(without alignments)
94.848 Million cell updates/sec

Title: US-09-647-457-2

Perfect score: 16

Sequence: 1 LVVGLCTCQIKTGPAC 16

Scoring table: OLIGO

Searched: 219241 segs, 76174552 residues

Word size: 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: PIR-68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	43.8	335	2 A39579	c-myc promoter-bin
2	7	43.8	395	2 I50026	phosphopyruvate hy
3	7	43.8	433	2 A23850	phosphopyruvate hy
4	7	43.8	433	2 A37210	phosphopyruvate hy
5	7	43.8	434	1 NOHUG	phosphopyruvate hy
6	7	43.8	434	1 NOMSB	phosphopyruvate hy
7	7	43.8	434	1 NOXL	phosphopyruvate hy
8	7	43.8	434	2 A24742	phosphopyruvate hy
9	7	43.8	434	2 SI0246	phosphopyruvate hy
10	7	43.8	434	2 SI0247	phosphopyruvate hy
11	7	43.8	434	2 A29170	phosphopyruvate hy
12	7	43.8	434	2 A32132	phosphopyruvate hy
13	7	43.8	434	2 S02072	phosphopyruvate hy
14	7	43.8	434	2 S06756	phosphopyruvate hy
15	7	43.8	434	2 UC4186	phosphopyruvate hy
16	7	43.8	434	2 UC4187	phosphopyruvate hy
17	7	43.8	434	2 JC1039	phosphopyruvate hy
18	7	43.8	434	2 A23126	phosphopyruvate hy
19	7	43.8	458	2 I37360	phosphopyruvate hy
20	6	37.5	142	2 S04071	hemoglobin alpha c
21	6	37.5	231	2 D64486	hypothetical prote
22	6	37.5	517	2 D86264	protein F3f19.6 (1
23	6	37.5	727	2 T10616	hypothetical prote
24	5	31.2	34	2 C43853	phosphopyruvate hy
25	5	31.2	72	2 T00181	hypothetical prote
26	5	31.2	73	2 T30612	hypothetical prote
27	5	31.2	85	2 H69191	hypothetical prote
28	5	31.2	88	2 C64697	flagellar biosynth
29	5	31.2	88	2 C82472	conserved hypothet

30	5	31.2	91	2 T45346	hypothetical prote
31	5	31.2	94	1 JC4508	flagellar biosynth
32	5	31.2	97	1 FEPR	ferredoxin [2Fe-2S
33	5	31.2	99	2 T40428	60S ribosomal prot
34	5	31.2	99	2 T43238	ribosomal protein
35	5	31.2	106	2 T45612	ferredoxin [2Fe-2S
36	5	31.2	110	2 C24775	T-cell receptor ga
37	5	31.2	111	2 G83480	cytochrome c ubiq
38	5	31.2	111	2 T09899	hypothetical prote
39	5	31.2	116	2 B75550	hypothetical prote
40	5	31.2	118	2 C84859	hypothetical prote
41	5	31.2	120	1 DER2N3	NADH dehydrogenase
42	5	31.2	120	2 S27251	NADH dehydrogenase
43	5	31.2	120	2 S58557	NADH dehydrogenase
44	5	31.2	121	2 T09244	plantacyanin precu
45	5	31.2	121	2 D84128	hypothetical prote

ALIGNMENTS

RESULT 1

A39579 c-myc promoter-binding protein MBP-1 - human

C/Species: Homo sapiens (man)

C/Date: 07-Feb-1992 #sequence revision 07-Feb-1992 #text_change 22-Jun-1999

C/Accession: A39579

R/Ray, R.; Miller, D.M.

Mol. Cell. Biol. 11, 2154-2161, 1991

A>Title: Cloning and characterization of a human c-myc promoter-binding protein.

A/Reference number: A39579; MUID:91172204

A/Accession: A39579

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-335 <RAY>

A/Cross-references: GB:M55914; NID:g180662; PIDN:AAA35698.1; PID:g180663

C/Genetics:

A/Gene: GDB:MBP1

A/Cross-references: GDB:127383

A/Map position: 8p11.2-8p11.1

C/Superfamily: enolase

C/Keywords: DNA binding; nucleus; transcription regulation

Query Match 43.8%; Score 7; DB 2; Length 335;

Best Local Similarity 100.0%; Pred. No. 2.6;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7
DB 285 LVVGLCT 291

RESULT 2

I50026 phosphopyruvate hydratase (EC 4.2.1.11) alpha - American alligator (fragment)

N/Alternate names: alpha-enolase

C/Species: Alligator mississippiensis (American alligator)

C/Date: 21-Feb-1997 #sequence revision 21-Feb-1997 #text_change 22-Jun-1999

C/Accession: I50026

R/Redges, S.B.

Proc. Natl. Acad. Sci. U.S.A. 91, 2621-2624, 1994

A>Title: Molecular evidence for the origin of birds.

A/Reference number: A53470; MUID:94195794

A/Accession: I50026

A/Status: preliminary; nucleic acid sequence not shown; translation not shown; tra

A/Molecule type: mRNA

A/Residues: 1-395 <HBD>

A/Cross-references: GB:L28078; NID:g472796; PIDN:AAA53671.1; PID:g472797

C/Superfamily: enolase

C/Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 43.8%; Score 7; DB 2; Length 395;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7
|||||||
DB 362 LVVGLCT 368

RESULT 3
A:23850
phosphopyruvate hydratase (EC 4.2.1.11), skeletal muscle - chicken
N:Alternate names: enolase, skeletal muscle
C:Species: Gallus gallus (chicken)
C>Date: 22-Jul-1987 #sequence revision 22-Jul-1987 #text_change 17-Mar-1999
C:Accession: A23850; A60809
R:Russell, G.A.; Dunbar, B.; Fothergill-Gilmore, L.A.
Biochem. J. 236, 115-126, 1986
A:Title: The complete amino acid sequence of chicken skeletal-muscle enolase.
A:Reference number: A23850; MUID:87075592
A:Accession: A23850
A:Molecule type: protein
A:Residues: 1-433 <RUS>
R:Gibson, B.W.; Daley, D.J.; Williams, D.H.
Anal. Biochem. 169, 217-226, 1988
A:Title: Structural elucidation of N-terminal post-translational modifications by mass spectrometry

A:Reference number: A60809; MUID:88250539
A:Accession: A60809
A:Molecule type: protein
A:Residues: 1-9 <GIB>
C:Comment: Several tissue-specific enolase isoenzymes are found in vertebrates.
C:Superfamily: enolase
C:Keywords: acetylated amino end; carbon-oxygen lyase; gluconeogenesis; glycolysis; hydrolysis; modified site: acetylated amino end (Ser) #status experimental
F:19/Binding site: magnesium 2 (Ser) #status predicted
F:209/Active site: Glu #status predicted
F:244,292,317/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 43.8%; Score 7; DB 2; Length 433;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7
|||||||
DB 383 LVVGLCT 389

RESULT 4
A:37210
phosphopyruvate hydratase (EC 4.2.1.11) beta - rabbit
N:Alternate names: enolase beta
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Dec-1991 #sequence revision 30-Dec-1991 #text_change 05-Aug-1994
C:Accession: A37210
R:Chin, C.C.
J. Protein Chem. 9, 427-432, 1990
A:Title: The primary structure of rabbit muscle enolase.
A:Reference number: A37210; MUID:91113295
A:Accession: A37210
A:Molecule type: preliminary
A:Molecule type: protein
A:Residues: 1-433 <CHI>
C:Superfamily: enolase
C:Keywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase
F:1/Modified site: acetylated amino end (Ala) #status experimental

Query Match 43.8%; Score 7; DB 2; Length 433;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7
|||||||
DB 383 LVVGLCT 389

RESULT 5
A:37210
phosphopyruvate hydratase (EC 4.2.1.11) gamma - human
N:Alternate names: enolase gamma; neuron-specific enolase
C:Species: Homo sapiens (man)
C>Date: 31-Mar-1990 #sequence revision 31-Mar-1990 #text_change 18-Jun-1999
C:Accession: J00060; S16163; S02077; I56569; S02616; S38303
R:Oliva, D.; Barba, G.; Barbieri, G.; Giallongo, A.; Feo, S.
Gene 79, 355-360, 1989
A:Title: Cloning, expression and sequence homologies of cDNA for human gamma enolase.
A:Reference number: J00060; MUID:90006764
A:Accession: J00060
A:Molecule type: mRNA
A:Residues: 1-434 <OLV>
A:Cross-references: GB:M22349; NID:951119; PIDN:AA59554.1; PID:9182116; GB:M27833
R:Oliva, D.; Call, L.; Feo, S.; Giallongo, A.
Genomics 10, 157-165, 1991
A:Title: Complete structure of the human gene encoding neuron-specific enolase.
A:Reference number: S16163; MUID:91257823
A:Accession: S16163
A:Molecule type: DNA
A:Residues: 1-434 <OL2>
A:Cross-references: GB:X51956; NID:931164; PIDN:CAA36215.1; PID:931165
R:McLeese, S.M.; Dunbar, B.; Fothergill, J.E.; Hinks, L.J.; Day, I.N.M.
Eur. J. Biochem. 178, 413-417, 1988
A:Title: Complete amino acid sequence of the neuron-specific gamma isozyme of enolase.
A:Reference number: S02077; MUID:89091176
A:Accession: S02077
A:Molecule type: mRNA
A:Residues: 2-3, 'O', '5'-239, 'M', '241-434 <MCV>
A:Cross-references: EMBL:X13120; NID:931145; PIDN:CAA31512.1; PID:9930063
A:Note: Part of this sequence was confirmed by protein sequencing
A:Note: 264-Ala and 395-Ala were also found
R:Van Obergerghen, L.; Kamholz, J.; Bishop, J.G.
J. Neurosci. Res. 19, 450-456, 1988
A:Title: Human gamma enolase: isolation of a cDNA clone and expression in normal and tumor cells
A:Reference number: I56569; MUID:88259288
A:Accession: I56569
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 'GC', '29-126', 'N', '128-434 <VAN>
A:Cross-references: GB:M27833; NID:9182117; PIDN:AA52388.1; PID:9182118
R:Day, I.N.M.; Allsopp, M.T.E.P.; Moore, D.C.M.; Thompson, R.J.
FEBS Lett. 222, 139-143, 1987
A:Title: Sequence conservation in the 3'-untranslated regions of neuron-specific enolase
A:Reference number: S02616; MUID:88005129
A:Accession: S02616
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 425-434 <DAY>
A:Cross-references: GB:Y00691; GB:M27833
R:Harrington, C.R.; Quinn, G.B.; Hurt, J.; Day, I.N.M.; Wischik, C.M.
Biochim. Biophys. Acta 1158, 120-128, 1993
A:Title: Characterisation of an epitope specific to the neuron-specific isoform of enolase
A:Reference number: S38303; MUID:94002176
A:Accession: S38303
A:Molecule type: protein
A:Residues: 156-173 <HAR>
C:Comment: Enolase occurs with at least three isoforms (alpha, beta, and gamma) in mammals
C:Comment: Thr-191 may be important for the enhanced tolerance to chloride ions of the gamma isoform
A:Gene: GDB:EN02
A:Cross-references: GDB:119872; OMIM:131360
A:Map position: 12p13-12p13
A:Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/2; 412/2
C:Complex: homodimer
C:Function:

A:Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phosphoenolpyruvate
A:Pathway: gluconeogenesis; glycolysis
C:Superfamily: enolase
C:Keywords: blocked amino end; brain; carbon-oxygen lyase; gluconeogenesis; glycolysis;
F:2.434/Product: phosphopyruvate hydratase gamma #status predicted <MA>
F:2/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #statu
F:40/Binding site: magnesium 2 (Ser) #status predicted
F:210,343/Active site: Glu, Lys #status predicted
F:245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 43.8%; Score 7; DB 1; Length 434;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7
DB 384 LVVGLCT 390

RESULT 6

NOMSB
phosphopyruvate hydratase (EC 4.2.1.11) beta - mouse
N:Alternate names: enolase beta
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 18-Jun-1999
C:Accession: S17109; S18036; S29675; A33921
R:Lamande, N.; Brosset, S.; Keller, A.; Lucas, M.; Lazar, M.
Submitted to the EMBL Data Library, September 1991
A:Reference number: S17109
A:Accession: S17109
A:Molecule type: DNA
A:Residues: 1-434 <LA>
A:Cross-references: EMBL:X61600; NID:g50848; PIDN:CAA43797.1; PID:g50849
R:Peterson, C.A.; Cho, M.; Rastlinejad, F.; Blau, H.M.
Submitted to the EMBL Data Library, October 1991
A:Description: Beta-enolase: a gene expressed in undifferentiated postnatal myoblasts th
A:Reference number: S18036
A:Accession: S18036
A:Molecule type: mRNA
A:Residues: 1-434 <PE>
A:Cross-references: EMBL:X62667; NID:g50143; PIDN:CAA44540.1; PID:g50144
R:Lazar, M.; Lamande, N.; Brosset, S.; Lucas, M.; Keller, A.
Submitted to the EMBL Data Library, February 1991
A:Reference number: S29675
A:Accession: S29675
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-434 <LA>
A:Cross-references: EMBL:X57247; NID:g50846; PIDN:CAA40913.1; PID:g50847
R:Lamande, N.; Marz, A.M.; Lucas, M.; Montarbo, D.; Pinset, C.; Gros, F.; Legault-Demar
Proc. Natl. Acad. Sci. U.S.A. 86, 4445-4449, 1989
A:Title: Murine muscle-specific enolase cDNA cloning, sequence, and developmental expre
A:Reference number: A33921; MUID:89282789
A:Accession: A33921
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 59-233; 'NA', 236-434 <LA>
A:Cross-references: GB:M20745; NID:g193029; PIDN:AAA37554.1; PID:g387144
A:Experimental source: skeletal muscle
C:Genetics:
A:Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2
C:Function:
A:Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phos
A:Pathway: gluconeogenesis; glycolysis
C:Superfamily: enolase
C:Keywords: carbon-carbon lyase; carbon-oxygen lyase; dimer; gluconeogenesis; glycolysis
F:40/Binding site: magnesium 2 (Ser) #status predicted
F:210,343/Active site: Glu, Lys #status predicted
F:245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 43.8%; Score 7; DB 1; Length 434;

Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7
DB 384 LVVGLCT 390

RESULT 7

NOMBL
phosphopyruvate hydratase (EC 4.2.1.11) ENOL - African clawed frog
N:Alternate names: enolase ENOL
C:Species: Xenopus laevis (African clawed frog)
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 18-Jun-1999
C:Accession: S00463
R:Segill, N.; Shrutkowski, A.; Dworkin, M.B.; Dworkin-Rastl, E.
Biochem. J. 251, 31-39, 1988
A:Title: Enolase isoenzymes in adult and developing Xenopus laevis and characteriz
A:Reference number: S00463; MUID:88268812
A:Accession: S00463
A:Molecule type: mRNA
A:Residues: 1-434 <SBG>
A:Cross-references: EMBL:Y00718; NID:g64679; PIDN:CAA68706.1; PID:g64680
C:Genetics:
A:Gene: ENOL
C:Function:
A:Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to
A:Pathway: gluconeogenesis; glycolysis
C:Superfamily: enolase
C:Keywords: carbon-oxygen lyase; dimer; gluconeogenesis; glycolysis; hydro-lyase; F
F:40/Binding site: magnesium 2 (Ser) #status predicted
F:210,343/Active site: Glu, Lys #status predicted
F:245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 43.8%; Score 7; DB 1; Length 434;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7
DB 384 LVVGLCT 390

RESULT 8

A24742
phosphopyruvate hydratase (EC 4.2.1.11) gamma - rat
N:Alternate names: 2-phospho-glycerate dehydratase; enolase gamma; neuronal enolase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 22-Jun-1999
C:Accession: A24742; PQ0006
R:Sakimura, K.; Kushiyu, E.; Odani, S.; Takahashi, Y.
Proc. Natl. Acad. Sci. U.S.A. 82, 7453-7457, 1985
A:Title: Molecular cloning and the nucleotide sequence of cDNA for neuron-specific
A:Reference number: A24742; MUID:86042683
A:Accession: A24742
A:Molecule type: mRNA
A:Residues: 1-434 <SAK>
A:Cross-references: GB:M11931; NID:g204041; PIDN:AAA41119.1; PID:g204042
R:Sakimura, K.; Kushiyu, E.; Takahashi, Y.; Suzuki, Y.
Gene 60, 103-113, 1987
A:Title: The structure and expression of neuron-specific enolase gene.
A:Reference number: PQ0006; MUID:88152493
A:Accession: PQ0006
A:Molecule type: DNA
A:Residues: 1-28 <SAK>
A:Cross-references: GB:M22770; GB:M18742; NID:g205766; PIDN:AAA41725.1; PID:g554480
C:Superfamily: enolase
C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match 43.8%; Score 7; DB 2; Length 434;
Best Local Similarity 100.0%; Pred. No. 3.2;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGICT 7
|||||
Db 384 LVVGICT 390

RESULT 9

S10246

phosphopyruvate hydratase (EC 4.2.1.11) alpha - mouse

N:Alternate names: 2-phosphoglycerate dehydratase; enolase alpha

C:Species: Mus musculus (house mouse)

C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 22-Jun-1999

C:Accession: S10246; A56781

R:Kaghad, M.; Dumont, X.; Chalou, P.; Lelias, J.M.; Lamande, N.; Lucas, M.; Lazar, M.; C

Nucleic Acids Res. 18, 3638, 1990

A:Title: Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from mouse brain.

A:Reference number: S10246; MUID:90301487

A:Accession: S10246

A:Molecule type: mRNA

A:Residues: 1-434 <RAG>

A:Cross-references: EMBL:X53328; NID:955490; PIDN:CAA36605.1; PID:955491

R:Bottillo, L.A.; Kendrick, N.C.; Keller, A.; Li, Y.; Tabas, I.

Arterioscler. Thromb. 13, 264-275, 1993

A:Title: Cholesteryl ester loading of mouse peritoneal macrophages is associated with ch

soform

A:Reference number: A56781; MUID:93152553

A:Accession: A56781

A:Status: preliminary

A:Molecule type: protein

A:Residues: 'X', 60, 'X', 62-67, 'X', 69-71, 'XX', 100-109, 'X', 111-112, 'X', 114, 'X', 184-185, 'X',

A:Experimental source: peritoneal macrophages

A:Note: sequence modified after extraction from NCBI backbone

A:Superfamily: enolase

C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match

Best Local Similarity 43.8%; Score 7; DB 2; Length 434;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGICT 7
|||||

Db 384 LVVGICT 390

RESULT 10

S10247

phosphopyruvate hydratase (EC 4.2.1.11) gamma - mouse

N:Alternate names: 2-phosphoglycerate dehydratase; enolase gamma

C:Species: Mus musculus (house mouse)

C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 22-Jun-1999

C:Accession: S10247

R:Kaghad, M.; Dumont, X.; Chalou, P.; Lelias, J.M.; Lamande, N.; Lucas, M.; Lazar, M.; C

Nucleic Acids Res. 18, 3638, 1990

A:Title: Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from mouse brain.

A:Reference number: S10246; MUID:90301487

A:Accession: S10247

A:Molecule type: mRNA

A:Residues: 1-434 <RAG>

A:Cross-references: EMBL:X52380; NID:955494; PIDN:CAA36606.1; PID:955495

C:Superfamily: enolase

C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match

Best Local Similarity 43.8%; Score 7; DB 2; Length 434;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGICT 7
|||||

Db 384 LVVGICT 390

RESULT 11

A29170

phosphopyruvate hydratase (EC 4.2.1.11) alpha - human

N:Alternate names: 2-phosphoglycerate dehydratase; enolase 1; enolase alpha

C:Species: Homo sapiens (man)

C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Jun-2000

C:Accession: S11696; A29170; S52858; A39183

R:Giallongo, A.; Feo, S.; Moore, R.; Croce, C.M.; Shove, L.C.

Eur. J. Biochem. 190, 567-573, 1990

A:Title: Structure of the human gene for alpha-enolase.

A:Reference number: S11696; MUID:90323004

A:Accession: S11696

A:Molecule type: DNA

A:Residues: 1-434 <GTA>

A:Cross-references: EMBL:X16288; NID:931172; PIDN:CAA4360.1; PID:91167843

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1989

R:Giallongo, A.; Feo, S.; Moore, R.; Croce, C.M.; Shove, L.C.

Proc. Natl. Acad. Sci. U.S.A. 83, 6741-6745, 1986

A:Title: Molecular cloning and nucleotide sequence of a full-length cDNA for human F

A:Reference number: A29170; MUID:86313654

A:Accession: A29170

A:Molecule type: mRNA

A:Residues: 1-434 <GT>

A:Cross-references: GB:M4328; NID:9182113; PIDN:AAA52387.1; PID:9182114

A:Note: the authors translated the codon AAG for residue 193 as His

R:Walter, M.; Leidenberger, F.A.; Schwepp, K.W.; Berg, H.; Northmann, W.

submitted to the EMBL Data Library, February 1995

A:Description: Autoreactive epitopes within the human alpha-enolase and their recog

A:Reference number: S52858

A:Accession: S52858

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-251, 'S', 253-434 <NAL>

A:Cross-references: EMBL:X84907; NID:9693932; PIDN:CAA59331.1; PID:9693933

A:Experimental source: endometrium carcinoma cell line HEC-1B

R:Miles, L.A.; Dahlberg, C.M.; Plescia, J.; Felez, J.; Kato, K.; Plov, E.F.

Biochemistry 30, 1682-1691, 1991

A:Title: Role of cell-surface lysines in plasminogen binding to cells: identification

A:Reference number: A39183; MUID:91129243

A:Accession: A39183

A:Molecule type: protein

A:Residues: 170-182, 'I', 184, 'R', 186-190, 245-252 <MIL>

A:Gene: GDB: ENO1

A:Cross-references: GDB:119871; OMIM:172430

A:Map position: 1p36-1p36

A:Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2

C:Function:

A:Description: catalyzes the reversible hydration of phosphoenolpyruvate to 2-phosp

C:Superfamily: enolase

C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesium

F.2-434/Product: phosphopyruvate hydratase alpha #status predicted <MAN>

Query Match

Best Local Similarity 43.8%; Score 7; DB 2; Length 434;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGICT 7
|||||

Db 384 LVVGICT 390

RESULT 12

A52132

phosphopyruvate hydratase (EC 4.2.1.11) alpha - duck

N:Alternate names: enolase alpha; tau-crystallin

C:Species: Anas platyrhynchos (domestic duck)

C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 21-Jul-2000

C:Accession: A52132

R:Wistow, G.J.; Lietman, T.; Williams, L.A.; Stapel, S.O.; de Jong, W.W.; Horwitz,

J. Cell Biol. 107, 2729-2736, 1988
 A:Title: Tau-crystallin/alpha-enolase: one gene encodes both an enzyme and a lens struct
 A:Reference number: A92750; MUID:89079778
 A:Accession: A32132
 A:Molecule type: mRNA
 A:Residues: 1-434 <WIS>
 A:Cross-references: GB:X14195; NID:962455; PIDN:CAA32409.1; PID:962456
 A:Superfamily: enolase
 C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match 43.8%; Score 7; DB 2; Length 434;
 Best Local Similarity 100.0%; Pred. No. 3.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVGLCT 7
 |||||
 Db 384 LVVGLCT 390

RESULT 13

S02072
 phosphopyruvate hydratase (EC 4.2.1.11) beta - rat
 N:Alternate names: enolase beta; enolase, muscle-specific
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 22-Jun-1999
 C:Accession: S02072

R:Ohshima, Y.; Mitsui, H.; Takayama, Y.; Kushiya, E.; Sakimura, K.; Takahashi, Y.
 FEBS Lett. 242, 425-430, 1989

A:Title: cDNA cloning and nucleotide sequence of rat muscle-specific enolase (beta-beta
 A:Reference number: S02072; MUID:89121113
 A:Accession: S02072

A:Molecule type: mRNA

A:Residues: 1-434 <OHS>

A:Cross-references: EMBL:X00979; NID:957781; PIDN:CAA68788.1; PID:957782

A:Note: The sequence from Fig. 4 is inconsistent with that from Fig. 2 in having 40-Asp

C:Superfamily: enolase

C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; muscle

Query Match 43.8%; Score 7; DB 2; Length 434;
 Best Local Similarity 100.0%; Pred. No. 3.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVGLCT 7
 |||||
 Db 384 LVVGLCT 390

RESULT 14

S06756
 phosphopyruvate hydratase (EC 4.2.1.11) beta - human
 N:Alternate names: enolase beta; enolase, skeletal muscle; phosphopyruvate hydratase, m
 C:Species: Homo sapiens (man)
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 22-Jun-1999
 C:Accession: S06756; S14759; S15933; S33330; S08685; S31650

R:Peshavaria, M.; Hinks, L.J.; Day, I.N.M.
 Nucleic Acids Res. 17, 8862, 1989

A:Title: Structure of human muscle (beta) enolase mRNA and protein, deduced from a genom
 A:Reference number: S06756; MUID:90067857
 A:Accession: S06756

A:Molecule type: mRNA

A:Residues: 1-434 <PES>

A:Cross-references: EMBL:X16504; NID:931169; PIDN:CAA34513.1; PID:931170

R:Peshavaria, M.; Day, I.N.M.

Biochem. J. 275, 427-433, 1991

A:Title: Molecular structure of the human muscle-specific enolase gene (ENO3).

A:Reference number: S14759; MUID:91222137

A:Accession: S14759

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-434 <PE2>

A:Cross-references: EMBL:X55976

R:Call, L.; Feo, S.; Oliva, D.; Giallongo, A.
 Nucleic Acids Res. 18, 1893, 1990

A:Title: Nucleotide sequence of a cDNA encoding the human muscle-specific enolase

A:Reference number: S15933; MUID:90245587

A:Accession: S15933

A:Molecule type: mRNA

A:Residues: 1-84, 'A', 86-161, 'K', 163-434 <CAL>

A:Cross-references: EMBL:X51957; NID:934788; PIDN:CAA36216.1; PID:934789

R:Giallongo, A.; Venturella, S.; Oliva, D.; Barbieri, G.; Rubino, P.; Feo, S.

Eur. J. Biochem. 214, 367-374, 1993

A:Title: Structural features of the human gene for muscle-specific enolase. Differ

A:Reference number: S33330; MUID:93292497

A:Accession: S33330

A:Molecule type: DNA

A:Residues: 1-161, 'K', 163-434 <GIN>

A:Cross-references: EMBL:X56832; NID:931166; PIDN:CAA40163.1; PID:931167

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1

C:Genetics:

A:Gene: GDB:ENO3

A:Cross-references: GDB:119873; OMIM:131370

A:Map position: 17pter-17p12

A:Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2

C:Superfamily: enolase

C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; muscle;

Query Match 43.8%; Score 7; DB 2; Length 434;
 Best Local Similarity 100.0%; Pred. No. 3.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVGLCT 7
 |||||
 Db 384 LVVGLCT 390

RESULT 15

JC4186
 phosphopyruvate hydratase (EC 4.2.1.11) alpha chain - chicken
 N:Alternate names: alpha-2-phospho-D-glycerate hydrolase; enolase
 C:Species: Gallus gallus (chicken)
 C:Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000
 C:Accession: JC4186

R:Tanaka, M.; Maeda, K.; Nakashima, K.

J. Biochem. 117, 554-559, 1995

A:Title: Chicken alpha-enolase but not beta-enolase has a Src-dependent tyrosine-p

A:Reference number: JC4186; MUID:95355305

A:Accession: JC4186

A:Molecule type: mRNA

A:Residues: 1-434 <TAN>

A:Cross-references: DDBJ:D37900; NID:974175; PIDN:BA407132.1; PID:974176

A:Experimental source: brain

C:Comment: This is a glycolytic enzyme and multiple isoenzyme forms were reported y

rates for tyrosine phosphorylation in Rous sarcoma virus and is important in all t

C:Superfamily: enolase

C:Keywords: carbon-oxygen lyase; hydro-lyase; phosphoprotein

F:44/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 43.8%; Score 7; DB 2; Length 434;
 Best Local Similarity 100.0%; Pred. No. 3.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVGLCT 7
 |||||
 Db 384 LVVGLCT 390

Search completed: May 8, 2002, 11:47:42
 Job time: 112 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 8, 2002, 11:43:34 ; Search time 12.53 Seconds
(without alignments)
28.735 Million cell updates/sec

Title: US-09-647-457-2
Perfect score: 90
Sequence: 1 LVVGLCTCQIKTGPAC 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 21252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/prodata/2/1aa/5A.COMB.pep.*
- 2: /cgn2_6/prodata/2/1aa/5B.COMB.pep.*
- 3: /cgn2_6/prodata/2/1aa/6A.COMB.pep.*
- 4: /cgn2_6/prodata/2/1aa/6B.COMB.pep.*
- 5: /cgn2_6/prodata/2/1aa/PC10S.COMB.pep.*
- 6: /cgn2_6/prodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	46	51.1	45	1	US-07-973-652-1	Sequence 1, Appl
2	46	51.1	45	1	US-07-950-773-1	Sequence 1, Appl
3	43	47.8	661	1	US-08-232-538-12	Sequence 12, Appl
4	43	47.8	661	2	US-08-786-164-12	Sequence 12, Appl
5	43	47.8	687	1	US-08-232-538-6	Sequence 6, Appl
6	43	47.8	687	2	US-08-786-164-6	Sequence 6, Appl
7	43	47.8	758	2	US-08-874-678-1	Sequence 1, Appl
8	43	47.8	758	3	US-08-643-839-1	Sequence 1, Appl
9	43	47.8	758	4	US-09-051-363-24	Sequence 24, Appl
10	43	47.8	780	1	US-08-232-538-14	Sequence 14, Appl
11	43	47.8	780	2	US-08-786-164-14	Sequence 14, Appl
12	43	47.8	1311	1	US-08-340-011-5	Sequence 5, Appl
13	43	47.8	1311	3	US-08-901-710-5	Sequence 5, Appl
14	43	47.8	1338	2	US-08-750-141A-3	Sequence 3, Appl
15	43	47.8	1362	2	US-08-874-678-3	Sequence 3, Appl
16	43	47.8	1362	3	US-08-643-839-33	Sequence 33, Appl
17	41	45.6	45	2	US-08-824-379-2	Sequence 2, Appl
18	41	45.6	177	2	US-08-465-794-17	Sequence 17, Appl
19	41	45.6	177	3	US-09-049-813-17	Sequence 17, Appl
20	41	45.6	178	2	US-08-465-794-18	Sequence 18, Appl
21	41	45.6	178	3	US-09-049-813-18	Sequence 18, Appl
22	41	45.6	178	4	US-08-663-191A-4	Sequence 4, Appl
23	40.5	45.0	2556	1	US-08-185-432-17	Sequence 17, Appl
24	40.5	45.0	2556	1	US-08-083-590A-20	Sequence 20, Appl
25	40.5	45.0	2556	3	US-08-532-384-20	Sequence 20, Appl
26	39.5	43.9	2523	1	US-08-185-432-18	Sequence 18, Appl
27	39	43.3	95	4	US-09-177-249-273	Sequence 273, App

28	39	43.3	481	1	US-07-927-071-1	Sequence 1, Appl
29	39	43.3	481	6	5164481-1	Patent No. 5164481
30	39	43.3	689	4	US-09-117-249-2	Sequence 2, Appl
31	39	43.3	689	4	US-09-061-769A-2	Sequence 2, Appl
32	39	43.3	992	1	US-08-127-499A-1	Sequence 1, Appl
33	39	43.3	992	1	US-08-482-847-1	Sequence 1, Appl
34	39	43.3	1063	1	US-08-093-453B-3	Sequence 3, Appl
35	39	43.3	1063	1	US-08-127-499A-8	Sequence 8, Appl
36	39	43.3	1063	1	US-08-482-847-8	Sequence 8, Appl
37	38.5	42.8	615	6	5177197-51	Patent No. 5177197
38	38.5	42.8	410	6	5177197-1	Patent No. 5177197
39	38.5	42.8	1394	6	5177197-30	Patent No. 5177197
40	38	42.2	37	2	US-08-248-839C-65	Sequence 65, Appl
41	38	42.2	45	2	US-08-824-379-3	Sequence 3, Appl
42	38	42.2	307	4	US-09-049-672A-9	Sequence 9, Appl
43	38	42.2	461	1	US-08-385-228-2	Sequence 2, Appl
44	38	42.2	461	2	US-08-650-000-2	Sequence 2, Appl
45	38	42.2	461	4	US-08-476-862-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-07-973-852-1
Sequence 1, Application US/07973852
Patent No. 5376640
GENERAL INFORMATION:
APPLICANT: Miyazaki, Toshiyuki
APPLICANT: Motol, Hirofumi
APPLICANT: Kodama, Toshiaki
APPLICANT: Maeda, Tatsuhiro
APPLICANT: Tsujita, Takahiro
APPLICANT: Okuda, Hiromichi
TITLE OF INVENTION: LIPOLYTIC ENZYME INHIBITORS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/973,852
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/631,321
FILING DATE: 20-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 332884/1989
FILING DATE: 25-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 75600/1990
FILING DATE: 27-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 194782/1990
FILING DATE: 25-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5376640man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1327-014-0 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR

; COMPUTER READABLE FORM:

; COMPUTER READABLE FORM:

ZIP: 07065-0900
COMPUTER READABLE FORM.

; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,164
FILING DATE: 21-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mark Hand, J
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18888DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
TELEFAX: 908-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 661 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-786-164-12

Query Match 47.8%; Score 43; DB 2; Length 661;
Best Local Similarity 50.0%; Pred. No. 89;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 4 GLCTCQIKTGA 15
|||:::|
DB 281 GLYTCRVRSGPS 292

RESULT 5
US-08-232-538-6
Sequence 6, Application US/08232538
Patent No. 5712380
GENERAL INFORMATION:
APPLICANT: Thomas, Kenneth A.
APPLICANT: Kendall, Richard L.
TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL CELL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000 126 E Lincoln Avenue
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,538
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W.III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 188881A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

LENGTH: 687 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-232-538-6

Query Match 47.8%; Score 43; DB 1; Length 687;
Best Local Similarity 50.0%; Pred. No. 92;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 4 GLCTCQIKTGA 15
|||:::|
DB 307 GLYTCRVRSGPS 318

RESULT 6
US-08-786-164-6
Sequence 6, Application US/08786164
Patent No. 5861484
GENERAL INFORMATION:
APPLICANT: THOMAS, KENNETH A.
APPLICANT: KENDALL, RICHARD L.
TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: CELL GROWTH FACTOR
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,164
FILING DATE: 21-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mark Hand, J
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18888DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
TELEFAX: 908-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-786-164-6

Query Match 47.8%; Score 43; DB 2; Length 687;
Best Local Similarity 50.0%; Pred. No. 92;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 4 GLCTCQIKTGA 15
|||:::|
DB 307 GLYTCRVRSGPS 318

RESULT 7
US-08-874-678-1
; Sequence 1, Application US/08874678
; Patent No. 5952199
; GENERAL INFORMATION:
; APPLICANT: Davis-Smyth, Terri L.
; APPLICANT: Chen, Helen H.
; APPLICANT: Presta, Leonard
; TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL GROWTH FACTOR
; TITLE OF INVENTION: ACTIVITY, THEIR USES AND PROCESSES FOR THEIR PRODUCTION
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/874,678
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/643,839
; FILING DATE: 07-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-63291-1/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 758 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-874-678-1

Query Match 47.8%; Score 43; DB 2; Length 758;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 4 GLTCQIKTGA 15
|||:::|
Db 307 GLYTCRVRSGPS 318

RESULT 8
US-08-643-839-1
; Sequence 1, Application US/08643839
; Patent No. 6100071
; GENERAL INFORMATION:
; APPLICANT: Davis-Smyth, Terri L.
; APPLICANT: Chen, Helen H.
; APPLICANT: Presta, Leonard
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert

STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/643,839
FILING DATE: 07-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63291/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 758 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-643-839-1

Query Match 47.8%; Score 43; DB 3; Length 758;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 4 GLTCQIKTGA 15
|||:::|
Db 307 GLYTCRVRSGPS 318

RESULT 9
US-09-051-363-24
; Sequence 24, Application US/09051363
; Patent No. 6270993
; GENERAL INFORMATION:
; APPLICANT: Shibuya, Masabumi
; APPLICANT: Niwa, Makio
; APPLICANT: Matsumoto, Tomoe
; APPLICANT: Asano, Makoto
; APPLICANT: Segawa, Toshiaki
; TITLE OF INVENTION: VEGF-BINDING POLYPEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/051,363
; FILING DATE: 07-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP96/02906
; FILING DATE: 07-OCT-1996
; APPLICATION NUMBER: 8/211892 JP

FILED DATE: 23-JUL-1996
APPLICATION NUMBER: 7/296476 JP
FILING DATE: 07-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 06501/012001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 758 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-051-363-24

Query Match 47.8%; Score 43; DB 4; Length 758;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 15
Db 307 GLYTCRVRSGPS 318

RESULT 10
US-08-232-538-14
Sequence 14, Application US/08232538
Patent No. 5712380
GENERAL INFORMATION:
APPLICANT: Thomas, Kenneth A.
TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL CELL
GROWTH FACTOR
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000 126 E. Lincoln Avenue
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,538
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W. III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 188881A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 780 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-232-538-14

Query Match 47.8%; Score 43; DB 1; Length 780;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 15
Db 307 GLYTCRVRSGPS 318

RESULT 11
US-08-786-164-14
Sequence 14, Application US/08786164
Patent No. 5861484
GENERAL INFORMATION:
APPLICANT: THOMAS, KENNETH A.
APPLICANT: KENDALL, RICHARD L.
TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL
CELL GROWTH FACTOR
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,164
FILING DATE: 21-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mark Hand, J
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18888DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
TELEFAX: 908-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 780 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-786-164-14

Query Match 47.8%; Score 43; DB 2; Length 780;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 15
Db 307 GLYTCRVRSGPS 318

RESULT 12
US-08-340-011-5
Sequence 5, Application US/08340011
Patent No. 577675
GENERAL INFORMATION:
APPLICANT: Altalo, et al.
TITLE OF INVENTION: FLT4, A NOVEL RECEPTOR TYROSIN KINASE
NUMBER OF SEQUENCES: 20

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;; STREET: 6300 Sears Tower, 233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: United States of America
;; ZIP: 60606-6402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/340,011
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/959,951
;; FILING DATE: 09-OCT-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meyers, Thomas C.
;; REGISTRATION NUMBER: 36,989
;; REFERENCE/DOCKET NUMBER: 32267
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/474-6300
;; TELEFAX: 312/474-0448
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1311 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-340-011-5

Query Match 47.8%; Score 43; DB 1; Length 1311;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTQPA 15
|||:::|
DB 317 GLYTCRVRSGPS 328

RESULT 13
US-08-901-710-5
; Sequence 5, Application US/08901710
; Patent No. 6107046
; GENERAL INFORMATION:
; APPLICANT: Alltalo, Karl
; APPLICANT: Aprelikova, Olga
; APPLICANT: Pajusola, Katri
; APPLICANT: Armstrong, Elna
; APPLICANT: Korhonen, Jaana
; APPLICANT: Kaipainen, Arja
; APPLICANT: Matikainen, Marja-Terttu
; TITLE OF INVENTION: FLT4, A RECEPTOR TYROSINE KINASE, AND USES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/901,710
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/340,011
;; FILING DATE: 14-NOV-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/257,754
;; FILING DATE: 09-JUL-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/959,951
;; FILING DATE: 09-OCT-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Gass, David A.
;; REGISTRATION NUMBER: 38,153
;; REFERENCE/DOCKET NUMBER: 28113/33824
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/474-6300
;; TELEFAX: 312/474-0448
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1311 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-901-710-5

Query Match 47.8%; Score 43; DB 3; Length 1311;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTQPA 15
|||:::|
DB 317 GLYTCRVRSGPS 328

RESULT 14
US-08-750-141A-3
; Sequence 3, Application US/08750141A
; Patent No. 6011003
; GENERAL INFORMATION:
; APPLICANT: Charnock-Jones, David S.
; APPLICANT: Boocock, Christine A.
; APPLICANT: Sharkey, Andrew M.
; TITLE OF INVENTION: FLT-4-(FMS-LIKE TYROSINE KINASE),
; TITLE OF INVENTION: FLT-15, VARIANTS THEREOF USED AS GROWTH FACTOR INHIBITORS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,141A
; FILING DATE: 12-MAY-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1396-1-001
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1338 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-750-141A-3

Query Match 47.8%; Score 43; DB 3; Length 1338;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 4 GLCTCQIKTGA 15
|||:::|:
Db 307 GLYTCRVRSGPS 318

RESULT 15
US-08-874-678-33
; Sequence 33, Application US/08874678
; Patent No. 5952199
; GENERAL INFORMATION:
; APPLICANT: Davis-Smyth, Terri L.
; APPLICANT: Chen, Helen H.
; APPLICANT: Presta, Leonardo
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL GROWTH FACTOR
; TITLE OF INVENTION: ACTIVITY, THEIR USES AND PROCESSES FOR THEIR PRODUCTION
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/874,678
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/643,839
; FILING DATE: 07-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-63291-1/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 398-3249
; TELEFAX: (415) 781-1989
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1362 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-874-678-33

Query Match 47.8%; Score 43; DB 2; Length 1362;

Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 4 GLCTCQIKTGA 15
|||:::|:
Db 305 GLYTCRVRSGPS 316

Search completed: May 8, 2002, 11:45:27
Job time: 113 sec

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OM protein - protein search, using sw model

Run on: May 8, 2002, 11:45:29 ; Search time 12.46 seconds
(without alignments)
28.897 Million cell updates/sec

Title: US-09-647-457-2
Perfect score: 16
Sequence: 1 LVVGLCTCQIKTGPAC 16

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 212252 seqs, 22503292 residues

Word size: 0

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

Issued_Patents_AA: *
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep: *
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6: /cgn2_6/ptodata/2/1aa/Dackfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	31.2	12	1	US-08-363-475-3
2	5	31.2	20	3	US-08-658-857B-15
3	5	31.2	20	3	US-08-763-226C-15
4	5	31.2	20	4	US-09-307-200-15
5	5	31.2	43	2	US-08-488-161-60
6	5	31.2	43	3	US-09-273-685-60
7	5	31.2	43	5	PCT-US95-11934-60
8	5	31.2	88	3	US-08-513-974B-340
9	5	31.2	149	3	US-08-425-673-5
10	5	31.2	184	1	US-08-907-800A-2
11	5	31.2	215	1	US-08-431-080-22
12	5	31.2	215	2	US-08-938-534-22
13	5	31.2	248	1	US-08-674-168-32
14	5	31.2	248	3	US-08-985-908-11
15	5	31.2	248	3	US-08-852-730-24
16	5	31.2	248	4	US-09-353-133-3
17	5	31.2	248	5	PCT-US95-02455-3
18	5	31.2	288	3	US-09-335-409-18
19	5	31.2	288	3	US-09-335-409-19
20	5	31.2	311	4	US-08-961-083-184
21	5	31.2	326	1	US-09-413-231-8
22	5	31.2	326	4	US-08-293-563-7
23	5	31.2	327	3	US-08-513-974B-372
24	5	31.2	328	3	US-08-513-974B-39
25	5	31.2	328	4	US-08-513-974B-371
26	5	31.2	333	4	US-09-413-231-10
27	5	31.2	369	1	US-07-816-283-8

28	5	31.2	369	1	US-08-417-103-8
29	5	31.2	369	2	US-08-411-859-3
30	5	31.2	369	4	US-08-120-601B-9
31	5	31.2	369	4	US-08-387-707-9
32	5	31.2	385	3	US-08-053-866-2
33	5	31.2	388	1	US-08-087-772A-2
34	5	31.2	400	1	US-07-916-901-6
35	5	31.2	400	1	US-07-783-602C-1
36	5	31.2	400	1	US-08-351-473B-4
37	5	31.2	400	1	US-08-351-473B-5
38	5	31.2	400	4	US-08-450-962-4
39	5	31.2	400	4	US-08-450-962-6
40	5	31.2	405	1	US-08-351-473B-2
41	5	31.2	420	4	US-08-847-065-19
42	5	31.2	423	4	US-09-243-374-6
43	5	31.2	442	6	5310667-6
44	5	31.2	444	1	US-08-476-008-51
45	5	31.2	444	1	US-08-476-008-52

ALIGNMENTS

RESULT 1
US-08-363-475-3
; Sequence 3, Application US/08363475
; Patent No. 5516679
GENERAL INFORMATION:
APPLICANT: Chiang, Shu-Ten
APPLICANT: Burnett Jr., William V.
TITLE OF INVENTION: PENICILLIN V AMIDOHYDROLASE GENE FROM
TITLE OF INVENTION: FUSARIUM OXYSPOREUM
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas R. Savitsky
STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,475
FILING DATE: 23-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Savitsky, Thomas R.
REGISTRATION NUMBER: 31,661
REFERENCE/DOCKET NUMBER: ON-0134
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 252 4526
TELEFAX: (609) 252 4526
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 8
OTHER INFORMATION: /note= "amino acid 8 can be ser or
; OTHER INFORMATION: Lys"
US-08-363-475-3
Query Match 31.2%; Score 5; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 KTGPA 15
11111
Db 3 KTGPA 7

RESULT 2

US-08-658-857B-15
; Sequence 15, Application US/08658857B
; Patent No. 6040435
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,857B
; FILING DATE: May 31, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/460,464
; FILING DATE: June 2, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07420/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-658-857B-15

Query Match 31.2%; Score 5; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 KTGPA 15
11111
Db 12 KTGPA 16

RESULT 3

US-08-763-226C-15
; Sequence 15, Application US/08763226C
; Patent No. 6057291
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla

STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/763,226C
FILING DATE: 10-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/658,857
FILING DATE: 31-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07420/014001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-763-226C-15

Query Match 31.2%; Score 5; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 KTGPA 15
11111
Db 12 KTGPA 16

RESULT 4

US-09-307-200-15
; Sequence 15, Application US/09307200
; Patent No. 6297215
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/307,200
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/763,226
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07420/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 15;
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-307-200-15

Query Match 31.2%; Score 5; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 KTGPA 15
|||||
Db 12 KTGPA 16

RESULT 5
US-08-488-161-60
Sequence 60, Application US/08488161
Patent No. 5885377
GENERAL INFORMATION:
APPLICANT: Alvarez, Vernon L.
TITLE OF INVENTION: Antigen Binding Peptides (Ablides) From
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,161
FILING DATE: 07-JUN-1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-176
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNTE
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-488-161-60

Query Match 31.2%; Score 5; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 IKTGP 14
|||||
Db 39 IKTGP 43

RESULT 6
US-09-273-685-60
Sequence 60, Application US/09273685

Patent No. 6015561
GENERAL INFORMATION:
APPLICANT: Alvarez, Vernon L.
TITLE OF INVENTION: Antigen Binding Peptides (Ablides) From
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/273,685
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,161
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-176
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNTE
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-273-685-60

Query Match 31.2%; Score 5; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 IKTGP 14
|||||
Db 39 IKTGP 43

RESULT 7
PCT-US95-11934-60
Sequence 60, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Ablides) From
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-11934-60

Query Match 31.2%; Score 5; DB 5; Length 43;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 IKTGP 14
|||||
DB 39 IKTGP 43

RESULT 8
US-08-513-974B-340
Sequence 340, Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiko
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 340:
SEQUENCE CHARACTERISTICS:
LENGTH: 88 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-513-974B-340

Query Match 31.2%; Score 5; DB 3; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VGLCT 7
|||||
DB 66 VGLCT 70

RESULT 9
US-08-425-673-5
Sequence 5, Application US/08425673
Patent No. 5508261
GENERAL INFORMATION:
APPLICANT: Moyie, William R.
APPLICANT: Campbell, Robert K.
TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
TITLE OF INVENTION: Methods For Preparing and Using Same
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard R. Muccino
STREET: P.O. Box 1267
CITY: Princeton
STATE: New Jersey
COUNTRY: USA
ZIP: 08551
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,673
FILING DATE:
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/717,151
FILING DATE: 18-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Muccino, Richard R.
REGISTRATION NUMBER: 32,538
REFERENCE/DOCKET NUMBER: UMD 1.0-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 466-3407
TELEFAX: (609) 466-2760
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-425-673-5

Query Match 31.2%; Score 5; DB 1; Length 149;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CQIKT 12
|||||
DB 93 CQIKT 97

RESULT 10

US-08-907-800A-2
Sequence 2, Application US/08907800A
Patent No. 6001646

GENERAL INFORMATION:

APPLICANT: SUN, Tung-tien
TITLE OF INVENTION: METHOD AND VECTOR FOR EXPRESSION AND
ISOLATION OF BIOLOGICALLY ACTIVE MOLECULES IN URINE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/907,800A
FILING DATE: 08-AUG-1997
CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/464,961
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: SUN-9A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-5528

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-907-800A-2

Query Match 31.2%; Score 5; DB 3; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVYGL 5
|||||
DB 170 LVYGL 174

RESULT 11

US-08-431-080-22
Sequence 22, Application US/08431080
Patent No. 5698686

GENERAL INFORMATION:

APPLICANT: Gottschling, Daniel E.
APPLICANT: Singer, Miriam S.
TITLE OF INVENTION: Telomerase Compositions and Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,080
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SN 08/326,781
FILING DATE: October 20, 1994

GENERAL INFORMATION:

ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:155/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-431-080-22

Query Match 31.2%; Score 5; DB 1; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 IKTGP 14
|||||
DB 38 IKTGP 42

RESULT 12

US-08-938-534-22
Sequence 22, Application US/08938534
Patent No. 5916752

GENERAL INFORMATION:

APPLICANT: Gottschling, Daniel E.
APPLICANT: Singer, Miriam S.

;; TITLE OF INVENTION: Telomerase Compositions and Methods
;; NUMBER OF SEQUENCES: 32
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White & Durkee
;; STREET: P.O. Box 4433
;; CITY: Houston
;; STATE: TEXAS
;; COUNTRY: UNITED STATES OF AMERICA
;; ZIP: 77210
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/938,534
;; FILING DATE: 26-SEP-1997
;; CLASSIFICATION: 536
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 08/431,080
;; FILING DATE:
;; APPLICATION NUMBER: SN 08/326,781
;; FILING DATE: October 20, 1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Parker, David L.
;; REGISTRATION NUMBER: 32,165
;; REFERENCE/DOCKET NUMBER: ARCD.155/PAR
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (512) 418-3000
;; TELEFAX: (713) 789-2679
;;
;; TELEX: 79-0924
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 215 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
US-08-938-534-22

Query Match 31.2%; Score 5; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 IKTGP 14
Db 38 IKTGP 42

RESULT 13
US-08-674-168-32
; Sequence 32, Application US/08674168
; Patent No. 5804414
; GENERAL INFORMATION:
; APPLICANT: MORIYA, Mika
; APPLICANT: MATSUI, Hiroshi
; APPLICANT: YOKOZAKI, Kenzo
; APPLICANT: HIRANO, Seiko
; APPLICANT: HAYAKAWA, Atsushi
; APPLICANT: IZUI, Masako
; APPLICANT: SUGIMOTO, Masakazu
; TITLE OF INVENTION: METHOD OF AMPLIFYING GENE USING
; TITLE OF INVENTION: ARTIFICIAL TRANSPOSON
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1735 JEFFERSON DAVIS HIGHWAY, SUITE # 400
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/674,168
;; FILING DATE: 01-JUL-1996
;; CLASSIFICATION: 435
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: JP 7-166541
;; FILING DATE: 30-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OBION, NORMAN F.
;; REGISTRATION NUMBER: 24,618
;; REFERENCE/DOCKET NUMBER: 10-810-0
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 413-3000
;; TELEFAX: (703) 413-2220
;; TELEX: 248855 OPAT UR
;; INFORMATION FOR SEQ ID NO: 32:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 248 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
US-08-674-168-32

Query Match 31.2%; Score 5; DB 1; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGL 5
Db 238 LVVGL 242

RESULT 14
US-08-985-908-11
; Sequence 11, Application US/08985908
; Patent No. 6004773
; GENERAL INFORMATION:
; APPLICANT: MASAYUKI ARAKI, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI
; TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1735 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,908
; FILING DATE: 05-DEC-1997
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 8-325659
; FILING DATE: 05-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: NORMAN F. OBION
; REGISTRATION NUMBER: 24,618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-985-908-11

Query Match 31.2%; Score 5; DB 3; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGL 5
|||||
Db 238 LVVGL 242

RESULT 15
US-08-852-730-24
Sequence 24, Application US/08852730
Patent No. 6090597
GENERAL INFORMATION:
APPLICANT: SEIKO HIRANO, MASAKAZU SUGIMOTO, EIICHI NAKANO,
APPLICANT: MASAKO IZUT, ATSUSHI HAYAKAWA, YASUHIKO YOSHIMURA, AND TSUYOSHI
APPLICANT: NAKAMATSU
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER AND NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
ZIP: 22026
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,730
FILING DATE: 05-07-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-142812
FILING DATE: 05-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-852-730-24

Query Match 31.2%; Score 5; DB 3; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGL 5
|||||
Db 238 LVVGL 242

Search completed: May 8, 2002, 11:47:22
Job time: 113 sec

